

**REMARKS/ARGUMENTS**

Claim 20, which was previously dependent from claim 15, has been re-written to be dependent from claim 15 once again. The scope of claim 20 is intended to be returned to that of original claim 20 with the limitations from claim 15, which were presented for business considerations and to better tailor the claims to encompass commercially contemplated embodiments of the invention at the present time rather than in acquiescence to any rejection asserted by the U.S. Patent and Trademark Office (PTO). Support is provided at least by claim 20 as originally filed and claim 15.

Claims 42 and 43 have been canceled without prejudice for pursuit in a continuing application.

No new matter has been introduced, and entry of the amendments is respectfully requested.

**Telephonic Interview of 2 March 2005**

Applicants thank Examiners Zeman and SPE A. Marschal for the courtesy of a telephonic interview on 2 March 2005 with them and Nicole Verona, Esq., of the assignee of interest in the instant application, and the undersigned as participants. The interview began with a discussion of the asserted anticipation rejection based upon the patent to Hung (U.S. Patent 6,642,009). The undersigned pointed out that of all the "markers" disclosed by Hung, no combination of five or more of them that would overlap with the genes disclosed in the instant application. Examiner Zeman indicated that she would review this argument in a written response more closely in combination with the arguments, in the response filed 8 September 2004, traversing this same rejection.

The undersigned also pointed out Applicants' understanding that the assertion of Hung under 35 U.S.C. § 102(e) based on the disclosure therein (as opposed to the claims) inherently includes the assertion that Hung placed his disclosed subject matter in the possession of the skilled artisan. This is in the absence of any disclosure of the nucleic acid sequence of any of the Hung "markers". Thus Hung is being relied upon as providing possession of his disclosed

subject matter to the skilled artisan via a written description that does not include specific sequences.<sup>1</sup> This is in contrast to the instant application where the absence of nucleic acid sequence disclosure has been asserted as resulting in a failure “to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.” The undersigned pointed out that the requirements of the same standard of “possession” appeared to be different between what is required of the Hung reference and what is required of the instant application.

The interview then turned to the asserted rejection under 35 U.S.C. § 112, first paragraph. The undersigned presented information from the IMAGE Consortium website explaining how each “clone ID” was a unique reference identifier that identified a particular nucleic acid molecule clone. There was also an explanation of how these unique “clone ID” identifiers were included in various publicly accessible sequence databases, such as GenBank and dBest. The undersigned then presented Applicants’ view that an adequate written description of the claimed invention was already present in the instant application because all the disclosed genes, as well as the particular nucleic acid molecule clones and associated sequences, were *already known in the art* (as evidenced by the clone ID reference numbers used and the availability of sequence information from publicly accessible sources). The undersigned also pointed out that this assertion of an adequate written description is consistent with the inherent assertion (explained above) that the Hung specification placed the Hung disclosed subject matter into the possession of the skilled person.

The Examiners maintained the position that inclusion of sequence information for each disclosed gene or clone ID was necessary for an adequate written description. They further indicated that amendments to the instant specification to include sequences for each disclosed gene/clone ID as known at the time of the invention would not introduced new matter. SPE Marschal also indicated that inclusion of any updated or corrected sequence for each disclosed gene/clone ID would also not introduce new matter.

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<sup>1</sup> Of course this discussion of an adequate disclosure of Hung’s subject matter in the Hung reference does not alter Applicants’ view that the Hung reference does not affect the patentability of the instant application’s pending claims.

The undersigned stated that Applicants would consider the possibility of amending the specification to include sequence information. However, the undersigned also expressed Applicants' view that the Examiners' requirement for inclusion of known sequence information for each gene/clone ID (as described above) would simply be an exercise of including information that was known in the art at the time of the invention. Because it is axiomatic that knowledge known in the art does not have to be included for an adequate written description, the undersigned questioned the Examiners' position that inclusion of the sequence information (which is just knowledge known in the art) is needed for an adequate written description. The Examiners only responded by indicating that sequence information would provide information regarding sequences that could be used in the invention.

Claim Rejection under 35 USC § 112, first paragraph

Claims 15-21, 30-41 and 44-48 were rejected under 35 USC § 112, first paragraph as allegedly "failing to comply with the written description requirement." Specifically, the statement of the instant rejection alleges that the claims contain "subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention."

Applicants have carefully considered the results of the interview as summarized above and reviewed the statement of the instant rejection. Applicants will consider the option of revising the application to include sequence information as described above, and Applicants expressly reserve the right to do so.

Before addressing the statement of this rejection, Applicants respectfully wish to provide further information regarding the public knowledge and availability of the genes disclosed in the instant application. Specifically, the IMAGE Consortium discloses how clones of the disclosed genes are as available from the American Type Culture Collection, Manassas, VA (ATCC). This is shown in attached Appendix 1, which has a screenshot of a page from the IMAGE Consortium website (at <http://image.llnl.gov/image/html/idistributors.shtml>), specifically pointing out multiple available sources for the clones. This is confirmed by the

ATCC website home page, where the top and bottom of the page are shown via two screenshots in Appendix 1. The second screenshot include a section entitled "Clone searching" which states

Finding the clone you need is easier than ever. Our new clone search allows you to search specifically by GenBank accession number, I.M.A.G.E. clone ID, or ATCC number. Look for a single clone or submit your entire list. We also offer a full range of clone plates and plate sets.  
[at <http://www.atcc.org/Home.cfm>]

The last screenshot in Appendix 1 is of the top of the clone search page at the ATCC website, which allows for searches based on IMAGE Consortium cloneID numbers. Based on the above, Applicants respectfully submit that no issue of public availability of the clones is present. The clones can readily be ordered and obtained and then used. The sequence inherent to each clone can be determined as desired. Accordingly, Applicants believe that an adequate written description is present without the need for sequence information in the instant application.

Applicants now turn to the statement of the instant rejection and their traversal thereof because they believe no *prima facie* case of an inadequate written description has been presented.

As noted above in the description of the interview, Applicants do not understand why the inclusion of sequence information known in the field (and publicly available) at the time of the invention is requested for an adequate written description.

The statement of the rejection asserts that "[a]rguing both the written description and art rejections together is inappropriate, as each rejection is assessed on its own merit." Applicants respectfully disagree with the above at least in situations like the instant application, where the inconsistent standards for *possession* by the skilled person as applied in the prior art rejection and *possession* by the skilled person as applied in the written description rejection are inconsistent. Applicants respectfully submit that it is inappropriate and arbitrary to apply one level of the *possession* test in the prior art rejection and another level in the instant rejection.



The statement of the rejection asserts that the instant “specification does not provide enough information for one of skill in the art to be able to obtain the proper sequences of the allegedly identified genes in order to make the arrays required.” Applicants respectfully disagree because contrary to the assertion, the skilled person can obtain sequence information about the genes identified in the instant application by use of the cloneID reference and/or the description of the gene. Information is available on both the IMAGE Consortium website as well as sequence database websites like GenBank as described above, where sequence information is indexed by cloneID identifiers. Additionally, the actual clones of each cloneID are publicly accessible as explained by the IMAGE Consortium, which even addresses the issue of clones that are no longer available because of the redundancy with other clones, which would of course be the replacement for an unavailable clone based on the redundancy.

Additionally, Applicants point out that the skilled person only needs to identify *the expression* of the genes disclosed in the instant application. As such, a partial sequence, as well as a sequence with enough complementarity to serve as a specific probe for the expression of the disclosed genes, is sufficient to be used in the practice of the claimed invention, such as by use of a probe containing array. There is simply no requirement to use the whole of the disclosed genes to detect their expression. Indeed, the instant application includes the recognition that it is not the particular sequences of the genes that is relevant but the identification of the expression of the genes as being correlated with stages of breast cancer. In the alternative, of course, an entire clone of one, or more, of the disclosed genes can be used to detect its, or their, expression.

The statement of the rejection also asserts that the “CloneID numbers are referencing a non-stable website which does not provide adequate written description of the reference sequences.” Applicants respectfully disagree because it is not clear as to what issue is raised by the alleged “non-stable” nature of the website. There is no indication that the cloneID identifiers are unstable with respect to specific clones. Moreover, the possibility that the sequence information associated with each cloneID identifier may be “non-stable” is irrelevant, because the nature of the actual clone remains constant. Applicants respectfully submit that the written description requirement in the instant application should be focused on the actual subject

of the genes (and detecting the expression thereof) rather than on merely a view of the genes. Stated differently, the written description requirement should be focused on the actual gene or genes, the expression of which is/are detected, rather than on the perception of what sequence to detect. This is emphasized by the fact that the invention can be practiced with use of the disclosed genes (via the disclosed clones) to be detected without actually knowing the particular sequence of the clone used.

The statement of the rejection further asserts that the disclosed sequences are not related in sequence or function and so “there is no structural or functional basis for identifying what sequences could be used in the invention.” While the Examiner may be correct in that many of the disclosed genes are unrelated in terms of their sequence, Applicants respectfully point out that the instant invention is based in part on the discovery of a common functionality of the disclosed genes in the ability to determine breast cancer progression based on the expression of the genes. This is a definite and clear function that is common to the disclosed genes, which are a defined set based upon the specific tables in the instant application.

Applicants are not aware of any requirement in U.S. patent law for a disclosure of “why” or “how” the expression of the disclosed genes are correlated with breast cancer progression. Accordingly, any requirement for disclosure of a “structure-function” relationship or “mechanism” by which the disclosed genes function is misplaced.

In light of the above, Applicants respectfully submit that the instant rejection is misplaced and may be properly withdrawn.

#### Claim Rejections under 35 USC § 102

Claims 15-21, 30-41 and 44-48 were rejected under 35 USC § 102(e) as allegedly anticipated by Hung (USP 6,642,009). Applicants point out that claim 20 has been revised as presented above.

Based in part on the interview as described above, Applicants have prepared a summary of the “markers” disclosed by Hung. The following table provides an alphabetical listing of the “markers” disclosed by Hung along with the number (from column 6, line 58, to column 9, line 37) and/or location of the disclosure in the Hung document.

<b>Hung “marker” name/description</b>	<b>Numerical identifier from columns 6-9 of Hung or other Hung location identifier</b>
absorption of a marker (like iodide) [this is not disclosed as based on the expression of any gene]	31
apoptosis-related protein	18
Bcl-2 gene product	16
breast cancer associated gene (BRCA)	30
BU101 protein	10
CD66a	12
CDw60 protein	36
cell adhesion molecule 5.2 (CAM 5.2)	14
carcino embryonic antigen (CEA)	col. 1, line 44
complement regulatory protein CD 46	22
complement regulatory protein CD 59	23
c-raf kinase	11
E2F1	4
Fibroblast growth factor	32
G-actin	col. 4, line 61
Insulin-like growth factor-1 (IGF-1 protein)	34
KAI1/CD82	28
Kallikrein 6 (zyme/protease M/neurosin or polypeptide hK6)	39
KL-1	13
leptin	15
Lg	3

lipocalin NGAL	19
FRA3B site (loss of heterozygosity there at) [this is not disclosed as based on the expression of any gene]	26
loss of heterozygosity [this is not disclosed as based on the expression of any gene]	25
lysophosphatidic acid (LPA) or a receptor thereof	1
MAGUK/ZO-1	6
Mammary expressed enzymes (cytochrome P450s, catechol-O-methyltransferase, epoxide hydrolase, peroxidases, glutathione-S-transferases, N-acetyltransferases, and sulfotransferases)	37
Mammastatin protein or polypeptide	38
Maspin protein	35
MRP-1/CD9	27
nuclear matrix 23 (nm23)	17
FHIT gene	24
p53 gene	col. 4, line 61
palladin	2
prothymosin alpha (PTA)	8
Repressor of estrogen receptor activity (REA)	7
T1A12/mac 25	5
thymosin beta-15	20
TMS-1	29
TNF-related apoptosis-inducing ligand (TRAIL)	9
tumor amplified kinase STK15 (BTAK or aurora2)	21
Vascular endothelial growth factor (VEGF)	33

Tables 2-5 of the instant application have been revised to be in alphabetical order based on the Description of each gene disclosed therein. Copies of these alphabetically reordered Tables are attached to the end of this response as Attachment A.<sup>2</sup> A comparison of the above table to the alphabetically reordered Tables in the Appendix is facilitated by the ability to look alphabetically for the same name.

Applicants have performed previously this type of comparison and noted the results in the response filed 8 September 2004. Specifically, there are only four possible “markers” from Hung that are in common with the instant application. These are the nuclear matrix 23 (nm23) marker (in column 7, lines 63-67 of Hung and possibly in instant Table 2); the complement regulatory protein CD 59 marker (in column 8, lines 22-25 of Hung and possibly in instant Table 3); the catechol-O-methyltransferase marker (in column 9, line 20 of Hung and possibly in instant Tables 2, 4, and 5); and the kallikrein 6 marker (column 9, lines 31-37 of Hung and possibly in instant Tables 2, 3, and 4).

Thus even assuming *in arguendo*, and with the reservation that Hung possibly does not actually disclose the use of the genes of Tables 2, 3, 4 and 5 (disclosed in part via the cloneID identifiers), that the above Hung markers are those disclosed in the respectively identified Tables, there is still no disclosure of the use of five or more genes of any one of the Tables as required by the instant claims.

Therefore, Applicants respectfully submit that this rejection may be properly withdrawn.

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<sup>2</sup> The alphabetically reordered Tables have the same content as the corresponding Tables in the instant application with the following exception: cloneIDs that were not listed with a Description have been updated to include the Description available at the IMAGE Consortium website on March 4, 2005. These Descriptions do not change the inherent nature of the clone identified by the cloneID identifier. The Descriptions are in bold text in the alphabetically reordered Tables of the Appendix.

The Descriptions included by the update is solely for the purpose to facilitate the comparison of the information in the Tables to the Hung disclosure and is not intended to introduce new matter into the instant application.



Appl. No. 10/028,018  
Amdt. dated 5 March 2005  
Reply to Office Action of 6 January 2005


PATENT

**CONCLUSION**

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 858-350-6100.

Respectfully submitted,

  
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Reg. No. 44,461

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Attachments  
KL:ps  
60436260 v1

## Appendix 1



### The I.M.A.G.E. Consortium

*"Sharing resources to achieve a common goal - the discovery of all genes"*

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#### I.M.A.G.E. Consortium Distributors

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I.M.A.G.E. clones and associated products may be obtained from any of our authorized distributors. On-line ordering through the WWW (or by email) is encouraged. To aid us in tracking I.M.A.G.E. resource use, distributors periodically inform the I.M.A.G.E. Consortium of the number of clones sent to each user; however the specific clones (i.e. CloneIDs) ordered are considered a confidential matter between each distributor and their customers.

Within the United States, the distributors are:

- American Type Culture Collection, Manassas, VA
- Open Biosystems, Huntsville, AL
- Research Genetics/Invitrogen, Carlsbad, CA

In Europe, I.M.A.G.E. distributors are:

- MRC geneservice, Babraham, UK
- RZPD German Resource Center for Genome Research, Berlin Germany

For a complete listing of associated contact information, [click here](#).

A Good Faith Agreement governs the usage of I.M.A.G.E. clones and associated products. The wording of the original document was revised in 9/00; the current agreement is now available and covers all I.M.A.G.E. clones and products retroactive to the beginning of the project.

I.M.A.G.E. downloads and parses GenBank records to find entries regarding I.M.A.G.E. clones. Groups sequencing I.M.A.G.E. clones can help us with this task by trying to conform to a few standards with respect to the format they use when submitting sequences. A Genbank Suggested Format document gives further details.

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### Cell immortalization products

Our new cell immortalization products allow you to look beyond the limits of primary cells. We now offer immortalized cell lines or you can immortalize your own with our telomerase cDNA tools. The possibilities are endless.

### Microbial genome of the month

The genome of *Silicibacter pomeroyi* shows unique adaptations to its marine environment (Nature 432: 910-913, 2004). We have the culture and the DNA from this organism, the first member of a major heterotrophic clade to be sequenced. (Photo courtesy of James R. Henriksen, University of Georgia, and Frank Mayer, Universität Göttingen.)

### The means to an end

We've illustrated the intrinsic and extrinsic apoptosis pathways to show the genes associated with each step. You can follow links to NCBI gene data and learn about clone availability in ATCC's catalog. Apoptosis detection kits and related cell lines are also noted when appropriate.

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ATCC: The Global Bioresource Center - Microsoft Internet Explorer

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Products for stem cell research. These include fully characterized nonhuman embryonic stem (ES) cells and lineage- or tissue-specific neonatally derived stem cells from several species. In addition, we offer ES-qualified support products like feeder layer cells, media, sera, and reagents.


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### Clone searching


Finding the clone you need is easier than ever. Our new [clone search](#) allows you to search specifically by GenBank accession number, I.M.A.G.E. clone ID, or ATCC number. Look for a single clone or submit your entire list. We also offer a full range of [clone plates and plate sets](#).

### Cell lines and coronaviruses


Attention coronavirus researchers: ATCC has the Vero E6 cell line as well as coronaviruses from a variety of species. See our [list of related materials](#) for more information.



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### Search by Clone Identifier

When you complete your search you can proceed with online ordering or e-mail the list to yourself to be ordered later. Note that you must have your ATCC account number available to order. **Volume discounts** will be calculated automatically for orders of 30 or more clones which can be sent to you in either 96- or 384-well plates. Orders for fewer than 30 clones will be sent as standard test tube cultures and will not be eligible for reduced pricing.

Step 1 - Choose identifier.

Step 2 - Enter ID list.

☐ GenBank
☐ I.M.A.G.E.
☐ ATCC Number

Other identifiers?
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Enter or Copy/Paste ID list.  
(Use a comma, return, or tab as your delimiter.)

- OR -

Submit a text file of clone IDs separated by a comma, return, or tab.

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### Search by Keyword

Internet

4



## Appendix 2

The Tables provided below are alphabetically reordered versions, based on the Description of each gene disclosed therein, of Tables 2-5 of patent application 10/028,018. The Tables have no change in content with the following exception: cloneIDs that were not listed with a Description have been updated to include the Description available at the IMAGE Consortium website on March 4, 2005. These entries are in bold text in the alphabetically reordered Tables.

The inclusion of Descriptions for these cloneIDs is solely for the purpose to facilitate the comparison of the information in the Tables to the Hung disclosure and does not introduce new matter into the application.

**Table 2** (in alphabetical order)

<b>CloneID</b>	<b>Weight</b>	<b>Description</b>
770785	0.6613519	1,2-alpha-mannosidase IC
1574058	1.0651351	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
430614	0.476288	2,3-bisphosphoglycerate mutase
838366	0.702617	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)
713782	0.7484589	a disintegrin and metalloproteinase domain 15 (metargidin)
704254	0.6653635	a disintegrin and metalloproteinase domain 8
1738208	0.7565056	a disintegrin-like and metalloprotease (repolysin type) with thrombospondin type 1 motif, 4
488505	0.808712	accessory proteins BAP31/BAP29
1587863	0.4270229	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3- oxoacyl-Coenzyme A thiolase)
823930	0.5633774	actin related protein 2/3 complex, subunit 1A (41 kD)
1473922	0.7892502	actin related protein 2/3 complex, subunit 3 (21 kD)
340558	0.7791736	actin related protein 2/3 complex, subunit 5 (16 kD)
2549634	0.5572052	activator of S phase kinase
210862	0.4692392	acyl-Coenzyme A oxidase 1, palmitoyl
343607	0.5029133	AD-015 protein
323693	0.5975785	adaptor-related protein complex 1, sigma 1 subunit
788641	0.4703576	adaptor-related protein complex 1, sigma 2 subunit
739109	0.5874334	adaptor-related protein complex 2, sigma 1 subunit

796757	0.5585876	adaptor-related protein complex 3, sigma 1 subunit
279970	0.7040135	adenosine A2a receptor
327635	0.5368033	adenylate kinase 1
51532	0.6504769	ADP-ribosylation factor-like 6 interacting protein
712139	-1.4736508	ADP-ribosylation factor-like 7
46248	0.7510436	ADP-ribosyltransferase (NAD <sup>+</sup> ; poly (ADP-ribose) polymerase)
774446	0.4567242	adrenomedullin
2095066	-0.9972552	alcohol dehydrogenase 1C (class I), gamma polypeptide
814798	-1.2748689	aldehyde dehydrogenase 1 family, member A3
47853	0.4231314	aldehyde dehydrogenase 4 family, member A1
812105	0.4424976	ALL1-fused gene from chromosome 1q
1635320	-1.2878152	amiloride-sensitive cation channel 2, neuronal
2250839	0.4994848	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
505289	0.5080495	angiotensin II, type I receptor-associated protein
208718	-1.1498532	annexin A1
666879	-1.3624072	annexin A8
239568	0.661735	annexin A9
1435862	0.9500093	antigen identified by monoclonal antibodies 12E7, F21 and O13
1568825	0.5205165	Arg/Abl-interacting protein ArgBP2
767487	0.4729158	ariadne (Drosophila) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1
2110511	0.8471736	artemin
377275	-1.2665702	ataxia-telangiectasia group D-associated protein
782439	0.454474	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit e
815737	-1.1116223	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
825386	0.5487104	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1F0, subunit d
2018821	0.6205344	ATPase inhibitor precursor
754625	0.4236648	ATPase, Class II, type 9A
266312	0.4201146	ATPase, Cu <sup>++</sup> transporting, beta polypeptide (Wilson disease)

810725	0.8510425	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 21kD
813256	-1.0407652	ATP-binding cassette, sub-family B (MDR/TAP), member 1
767798	0.6192232	ATX1 (antioxidant protein 1, yeast) homolog 1
753897	0.5153412	autocrine motility factor receptor
244764	0.5424555	B7 homolog 3
796694	0.7317383	baculoviral IAP repeat-containing 5 (survivin)
1709791	1.0378948	BAI1-associated protein 1
1609665	-0.9851713	BarH-like homeobox 2
1456701	0.7934389	B-cell CLL/lymphoma 9
1565079	0.4415966	B-cell linker
2244196	0.6807351	B-cell receptor-associated protein BAP29
814899	0.5142481	BCL2/adenovirus E1B 19kD-interacting protein 3-like
2043167	0.7224903	BCL2-associated athanogene 3
1916575	0.4923447	BCL2-interacting killer (apoptosis-inducing)
1568561	0.4808662	BCL2-like 1
809357	0.7535411	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)
786069	-1.1143906	beta-site APP-cleaving enzyme
741977	0.7715372	B-factor, properdin
1420370	0.6531171	biliverdin reductase B (flavin reductase (NADPH))
empty-31	0.4726918	blank
1733262	0.6293971	BLu protein
811024	0.7117211	bone marrow stromal cell antigen 2
1616253	0.5190257	breast carcinoma amplified sequence 1
191904	0.6141265	BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog
781047	0.4699376	budding uninhibited by benzimidazoles 1 (yeast homolog)
271472	0.7901735	C3HC4-like zinc finger protein
754653	0.4707927	cadherin, EGF LAG seven-pass G-type receptor 3, flamingo (Drosophila) homolog
841679	0.6762195	calcium and integrin binding protein (DNA-dependent protein kinase interacting protein)
49630	0.6027878	calcium channel, voltage-dependent, L type, alpha 1D subunit
346134	0.5132068	calcium-regulated heat-stable protein (24kD)
772913	-1.0122192	calreticulin
785793	0.5072717	capping protein (actin filament) muscle Z-line, alpha 1

649084	0.5099122	carbonic anhydrase XI
67765	0.6967324	carboxypeptidase M
509823	0.6334191	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
744417	0.8409538	carnitine acetyltransferase
30170	0.4936252	caspase 3, apoptosis-related cysteine protease
72778	-1.3873177	caspase 7, apoptosis-related cysteine protease
1878409	-1.1144369	catechol-O-methyltransferase
51083	0.6544472	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)
345538	0.4550133	cathepsin L
842994	0.7563101	cathepsin Z
377461	-1.4787671	caveolin 1, caveolae protein, 22kD
1572298	-0.9906095	CD3Z antigen, zeta polypeptide (TiT3 complex)
725454	0.7335223	CDC28 protein kinase 2
786067	0.5361882	cell division cycle 25B
415102	0.5465851	cell division cycle 25C
376516	0.5906248	cell division cycle 4-like
2017415	0.5353408	centromere protein A (17kD)
366067	0.6416356	cerebellar degeneration-related protein (62kD)
1626996	-1.0328113	c-fos induced growth factor (vascular endothelial growth factor D)
2108077	0.7700354	CGI-112 protein
726439	0.5080059	CGI-143 protein
1947647	0.5064941	CGI-147 protein
753400	0.496254	CGI-204 protein
811774	1.0617336	CGI-49 protein
624667	0.7524325	CGI-92 protein
884425	0.5265114	chaperonin containing TCP1, subunit 5 (epsilon)
882484	0.6521026	chaperonin containing TCP1, subunit 7 (eta)
283023	-1.0825166	chemokine (C-X3-C) receptor 1
72050	0.5722845	chloride channel, nucleotide-sensitive, 1A
293569	0.5162069	chromosome 1 open reading frame 21
1492426	0.9397097	chromosome 19 open reading frame 3
824052	0.8650616	chromosome 6 open reading frame 1
469383	0.4607375	chromosome 8 open reading frame 1
731308	0.8166873	citrate synthase
124331	0.624455	cleavage and polyadenylation specific factor 5, 25 kD subunit

510794	0.4691467	c-myc binding protein
1656062	0.593408	coagulation factor XII (Hageman factor)
1632252	0.474559	complement component 1, q subcomponent, alpha polypeptide
2322079	0.4309341	contig C019549, human
127646	0.5838788	contig C030249, human
823909	0.4215098	contig C039966, human
770992	0.4346858	contig C056172, human
897770	0.4836347	contig C071196, human
108425	0.6761526	contig C076797, human
283751	0.4179154	cortistatin
489823	0.5666593	COX17 (yeast) homolog, cytochrome c oxidase assembly protein
1416782	0.5657017	creatine kinase, brain
839736	-1.4745405	crystallin, alpha B
1555924	-1.1342985	CSR1 protein
701751	0.6824676	cut (Drosophila)-like 1 (CCAAT displacement protein)
487444	0.4887966	cyclic AMP phosphoprotein, 19 kD
742595	0.8291965	cyclin-dependent kinase 5
700792	0.5493223	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
1323448	1.5470535	cysteine-rich protein 1 (intestinal)
360254	-1.0325653	cysteine-rich, angiogenic inducer, 61
196189	0.6338517	cytochrome b-5
1455394	0.4455695	cytochrome c
278531	0.6737637	cytochrome c oxidase subunit VIc
1601947	0.5744444	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
884511	0.4199518	cytochrome c oxidase subunit VIIb
38356	0.4173012	cytochrome P450, subfamily 46 (cholesterol 24-hydroxylase)
768064	0.7743382	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1
724888	0.4196322	cytochrome P450, subfamily IVB, polypeptide 1
810039	0.4491986	defender against cell death 1
296702	0.5162041	deiodinase, iodothyronine, type I
1492468	0.647846	DEME-6 protein
810156	0.6266313	deoxythymidylate kinase (thymidylate kinase)
1161564	-1.5917197	desmuslin
842980	0.7284256	developmentally regulated GTP-binding protein 1
795401	0.5264278	diacylglycerol O-acyltransferase (mouse) homolog



813387	0.5460577	diaphorase (NADH/NADPH) (cytochrome b-5 reductase)
760299	-1.8654555	dickkopf (Xenopus laevis) homolog 3
742685	-1.4440371	disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
767761	0.6142782	DKFZP434B168 protein
825740	0.5931142	DKFZp434J1813 protein
366353	0.7664569	DKFZP564C186 protein
770766	0.6193342	DKFZP564C1940 protein
345423	0.4538841	DKFZP564M112 protein
294397	0.5066683	DKFZP586A0522 protein
2011515	0.6774452	DKFZP586B0923 protein
202514	0.6872212	DNA (cytosine-5-)-methyltransferase 3 alpha
809466	0.5532437	DNA segment on chromosome 19 (unique) 1177 expressed sequence
754046	0.4550413	DNA segment on chromosome X (unique) 9879 expressed sequence
263727	0.5313082	DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis)
454896	0.4760701	DnaJ (Hsp40) homolog, subfamily A, member 2
1637302	0.424164	DNAJ domain-containing
2018527	0.599584	dolichyl-phosphate mannosyltransferase polypeptide 3
884462	-1.2078038	Down syndrome critical region gene 1
154610	0.4948571	dynactin 4
782688	0.4694868	dynein, axonemal, light intermediate polypeptide
593023	-1.0135883	dystrobrevin, beta
1864302	-1.0099902	E74-like factor 5 (ets domain transcription factor)
781017	-1.3232108	early growth response 2 (Krox-20 (Drosophila) homolog)
188335	-1.0161259	egf-like module containing, mucin-like, hormone receptor-like sequence 2
295986	0.5544422	emopamil-binding protein (sterol isomerase)
2248488	0.6337488	ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate)
1687976	0.4257058	endoplasmic reticulum chaperone SIL1, homolog of yeast
74070	0.4390933	endosulfine alpha
823574	0.5978052	endosulfine alpha
122147	0.4652151	<b>engulfment and cell motility 2 (ced-12 homolog, C. elegans) (ELMO2), Homo sapiens</b>
366834	0.5191005	envoplakin

153760	-1.1793765	EphB1
811088	-1.1625002	ephrin-B3
1577736	-1.035115	epidermal growth factor (beta-urogastrone)
109863	0.8066906	epithelial membrane protein 2
34093	-1.2156885	EST
594500	0.7935958	EST
1641894	0.5587185	EST
358267	0.6962436	EST, Moderately similar to AF119917 63 PRO2831 [H.sapiens]
34150	-1.0302576	ESTs
40027	-1.0057005	ESTs
41826	0.4264531	ESTs
70606	0.4475592	ESTs
83358	0.4397161	ESTs
139660	-1.0134677	ESTs
140635	0.4384907	ESTs
162308	-1.023071	<b>ESTs</b>
162308	-1.2006293	ESTs
196435	-1.2282733	ESTs
214996	0.45033	ESTs
250313	0.5649247	ESTs
266500	0.5135558	ESTs
281190	-0.9830533	ESTs
290101	0.4800598	ESTs
344091	0.6381862	ESTs
365738	0.7709456	ESTs
415816	-0.9954308	ESTs
564847	0.757516	ESTs
564981	0.6712134	ESTs
754628	0.7573763	ESTs
757191	-1.2902603	ESTs
784105	0.6003082	ESTs
814209	0.5736866	ESTs
827171	0.7211896	ESTs
855707	0.4456433	ESTs
1027283	0.4628012	ESTs
1257131	-1.1566479	ESTs
1500162	0.7571399	ESTs
1517749	0.5665848	ESTs
1536006	0.7499887	ESTs
1537001	0.4539586	ESTs
1557637	0.4705061	ESTs
1558233	0.5101529	ESTs
1585492	0.4571478	ESTs
1700436	0.6215741	ESTs

1899312	0.4418248	ESTs
2046679	0.4579596	ESTs
431505	0.6534315	ESTs, Highly similar to A31026 probable membrane receptor protein [H.sapiens]
289760	-1.5534789	ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]
79726	0.5078677	ESTs, Highly similar to T46395 hypothetical protein DKFZp434I1120.1 [H.sapiens]
279720	0.5645072	ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.sapiens]
725978	0.7010756	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
530197	0.6659784	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
593431	0.6578268	ESTs, Moderately similar to CEGT_HUMAN CERAMIDE GLUCOSYLTRANSFERASE [H.sapiens]
345670	-1.889471	ESTs, Moderately similar to I59348 CCAAT binding transcription factor CBF subunit C - rat [R.norvegicus]
529843	-1.2405917	ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]
120749	0.6172281	ESTs, Moderately similar to KIAA1215 protein [H.sapiens]
179212	0.4594831	ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]
160192	-1.4695435	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
2017721	0.4268089	ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]
810497	0.4572069	ESTs, Weakly similar to A35363 synapsin I splice form a [H.sapiens]
73009	0.516678	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
726699	0.6131491	ESTs, Weakly similar to AAB47496 NG5 [H.sapiens]
746163	0.4863317	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]

2016908	0.9615102	ESTs, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens]
488642	0.5560728	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
128695	0.4340119	ESTs, Weakly similar to I38344 titin, cardiac muscle [H.sapiens]
1640821	0.8544081	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
841621	0.4466003	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
742707	0.7955239	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens]
2029173	0.9672743	ESTs, Weakly similar to N-WASP [H.sapiens]
1583198	0.4350835	ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]
2572170	0.5852444	ESTs, Weakly similar to T26581 hypothetical protein Y32B12A.3 - Caenorhabditis elegans [C.elegans]
358936	0.6441198	ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]
743589	0.7372744	ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]
35147	1.3764654	ESTs, Weakly similar to unnamed protein product [H.sapiens]
488202	0.9501137	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens]
796542	-1.5553964	ets variant gene 5 (ets-related molecule)
811837	-1.1269309	<b>eukaryotic translation elongation factor 1 alpha 1</b>
811837	-1.1468554	eukaryotic translation elongation factor 1 alpha 1
469151	0.4622121	eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD )
74566	0.4279059	exportin 1. (CRM1, yeast, homolog)
301122	0.6299499	extracellular matrix protein 1
782503	0.4205398	fatty acid desaturase 1
1758590	0.6074571	fatty-acid-Coenzyme A ligase, long-chain 3
1469148	0.467634	FGFR1 oncogene partner

809464	0.426456	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)
752631	0.7139862	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
789012	0.6794432	fibulin 2
813616	0.5574238	FK506-binding protein like
376875	0.6286902	flavin containing monooxygenase 1
131839	-1.7087069	folate receptor 1 (adult)
772220	0.4475721	for protein disulfide isomerase-related
628955	-0.997687	forkhead box O1A (rhabdomyosarcoma)
796475	-1.0217348	four and a half LIM domains 3
52419	-1.2004086	Friedreich ataxia region gene X123
2309073	0.5617024	frizzled (Drosophila) homolog 5
298122	-1.5678888	frizzled (Drosophila) homolog 7
1499828	0.5479012	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)
183200	0.5801312	fumarylacetoacetate hydrolase (fumarylacetoacetase)
2016775	-1.0761731	G protein-coupled receptor, family C, group 5, member B
842825	0.7235007	G1 to S phase transition 1
1854539	0.4824023	GAP-associated tyrosine phosphoprotein p62 (Sam68)
214068	0.4383007	GATA-binding protein 3
1393018	0.701717	general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD )
741474	0.8925439	glucose phosphate isomerase
2018337	0.6828744	glucosidase, beta; acid (includes glucosylceramidase)
1609836	1.2349106	glutamate-ammonia ligase (glutamine synthase)
731044	0.8657953	glutaredoxin 2
1848977	0.5519913	glycerol kinase
344720	-1.7951928	glycophorin C (Gerbich blood group)
358217	0.4507923	glypican 4
686552	0.7506994	golgi phosphoprotein 1
1556433	-1.4191955	GRO3 oncogene
752643	0.5774681	group XII secreted phospholipase A2
85195	0.4207753	growth arrest and DNA-damage-inducible, gamma
796181	-1.1584587	growth arrest-specific 6
788654	0.8886269	<b>growth factor receptor-bound protein 2</b>
788654	1.4818381	growth factor receptor-bound protein 2



810063	0.8168926	growth factor, erv1 ( <i>S. cerevisiae</i> )-like (augmenter of liver regeneration)
51741	0.5795151	GTP-binding protein
308466	0.8803492	GTP-binding protein Sara
40773	0.4510289	guanine nucleotide binding protein (G protein), alpha z polypeptide
292213	0.5883092	guanine nucleotide binding protein (G protein), beta polypeptide 2
66317	0.5648355	H1 histone family, member 2
283919	1.118257	H2A histone family, member L
488964	1.1545223	H2A histone family, member O
290841	0.9562201	H2B histone family, member A
1500000	1.3204029	H2B histone family, member B
430235	0.585372	H2B histone family, member Q
815781	0.5340254	heat shock 105kD
471568	1.1466811	hematological and neurological expressed 1
1569187	-1.9090486	heparan sulfate (glucosamine) 3-O-sulfotransferase 4
345833	0.4187433	heterogeneous nuclear ribonucleoprotein A/B
770845	0.6253839	hexokinase 1
1637282	0.542121	hexokinase 2
345787	0.4734963	highly expressed in cancer, rich in leucine heptad repeats
172517	0.6701228	hippocalcin-like 1
1434948	0.4771454	HIV TAT specific factor 1
1434905	0.4382073	homeo box B7
347726	0.4837701	homeo box D8
1592715	0.6637095	Homer, neuronal immediate early gene, 3
742581	0.433453	Homo sapiens cDNA FLJ10366 fis, clone NT2RM2001420
1474424	0.6006702	Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328
212542	0.6938079	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321
270826	-1.0112851	Homo sapiens cDNA FLJ13329 fis, clone OVARC1001795
283739	0.5276555	Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838
366156	0.4563893	Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838
825327	0.7622414	Homo sapiens cDNA FLJ14105 fis, clone MAMMA1001202
35626	0.4509825	Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955

1492780	0.5555908	Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409
770675	0.4319407	Homo sapiens cDNA: FLJ21323 fis, clone COL02374
131094	0.9518372	Homo sapiens cDNA: FLJ21587 fis, clone COL06946
814528	0.9569471	Homo sapiens cDNA: FLJ22139 fis, clone HEP20959
753071	-1.8417236	Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
840266	-1.6530726	Homo sapiens cDNA: FLJ22667 fis, clone HSI08385
745394	0.4374406	Homo sapiens cDNA: FLJ23249 fis, clone COL04196
727078	0.7472345	Homo sapiens cDNA: FLJ23602 fis, clone LNG15735
823694	0.5321203	Homo sapiens chromosome 19, BAC CIT-HSPC_204F22 (BC228680), complete sequence; contains bacterial insertion element
649977	0.5002695	Homo sapiens clone CDABP0014 mRNA sequence
796723	1.0724133	Homo sapiens clone CDABP0014 mRNA sequence
488404	-1.1981268	Homo sapiens clone TUA8 Cri-du-chat region mRNA
768452	0.5237494	Homo sapiens EST from clone 491476, full insert
743977	0.5237158	Homo sapiens mRNA for TL132
327506	0.5092192	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 327506
70245	-1.0348655	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 50374
44292	0.8732235	Homo sapiens mRNA; cDNA DKFZp434C107 (from clone DKFZp434C107)
1871116	-1.0975491	Homo sapiens mRNA; cDNA DKFZp434C1714 (from clone DKFZp434C1714); partial cds
1883028	0.5828007	Homo sapiens mRNA; cDNA DKFZp434J1912 (from clone DKFZp434J1912)
2016648	0.8263671	Homo sapiens mRNA; cDNA DKFZp434N1728 (from clone DKFZp434N1728)
265103	0.6548137	Homo sapiens mRNA; cDNA DKFZp547M123 (from clone DKFZp547M123)

565319	1.2369212	Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DKFZp564B1264)
813265	-1.2549431	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)
486683	-1.6799604	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)
1844765	0.5670398	Homo sapiens mRNA; cDNA DKFZp564O1763 (from clone DKFZp564O1763)
1461477	0.509331	Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324)
1584540	-1.0077508	Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022)
132857	-1.0989746	Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone DKFZp586N1323)
22917	-1.5156635	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)
74738	0.5835427	Homo sapiens, clone IMAGE:3535294, mRNA, partial cds
1631735	0.7505843	Homo sapiens, clone IMAGE:3604336, mRNA, partial cds
186768	0.7298378	Homo sapiens, clone IMAGE:3604869, mRNA
292770	0.8570995	Homo sapiens, clone IMAGE:3627860, mRNA, partial cds
1652310	0.4512689	Homo sapiens, clone MGC:19613 IMAGE:3833049, mRNA, complete cds
810002	-1.7256692	Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds
810567	0.4702908	Homo sapiens, clone MGC:3182 IMAGE:3356293, mRNA, complete cds
121436	0.4691298	Homo sapiens, clone MGC:4677 IMAGE:3532809, mRNA, complete cds
1635665	0.5714089	Homo sapiens, RIKEN cDNA 2010100O12 gene, clone MGC:14813 IMAGE:4133274, mRNA, complete cds
491527	0.5116183	Homo sapiens, Similar to CG7083 gene product, clone MGC:10534 IMAGE:3957147, mRNA, complete cds
130835	0.4946783	Homo sapiens, Similar to clone FLB3816, clone IMAGE:3454380, mRNA

41123	0.481642	Homo sapiens, Similar to RIKEN cDNA 2210021G21 gene, clone MGC:14859 IMAGE:3621871, mRNA, complete cds
839746	0.5031787	Homo sapiens, Similar to RIKEN cDNA 5830420C20 gene, clone IMAGE:3633379, mRNA, partial cds
1492238	1.1991653	HSPC003 protein
1600239	0.421459	HSPC037 protein
796469	1.1850928	HSPC150 protein similar to ubiquitin-conjugating enzyme
772925	0.5940171	HSPCO34 protein
470099	0.7343404	HT002 protein; hypertension-related calcium-regulated gene
241043	0.5545302	Human clone 137308 mRNA, partial cds
813675	0.4614894	Human D9 splice variant B mRNA, complete cds
178805	1.2225746	Human DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to Drosophila Scratch (Scrt), Slug and Xenopus Snail, a novel gene similar to Drosophila CG6762, STSs, GSSs and five CpG
811585	0.7087617	huntingtin (Huntington disease)
1554549	1.1440029	hydroxyacyl glutathione hydrolase
813419	0.8043966	hydroxyacyl-Coenzyme A dehydrogenase, type II
256619	0.7395032	hydroxysteroid (17-beta) dehydrogenase 7
80764	0.6765616	hypothetical protein
139354	0.5318709	hypothetical protein
140289	0.6205892	hypothetical protein
595213	0.5775511	hypothetical protein
785766	0.6058332	hypothetical protein
810402	0.7407907	hypothetical protein
811848	-1.3549757	hypothetical protein
825822	0.5097808	hypothetical protein
841260	0.5285587	hypothetical protein
299815	0.5485843	hypothetical protein DC42
150118	0.4383146	hypothetical protein DKFZp434F054
32489	-1.0196444	hypothetical protein DKFZp566A1524
489351	0.65846	hypothetical protein DKFZp566J2046
746190	0.4291743	hypothetical protein DKFZp761B1514
76182	-1.2102812	hypothetical protein DKFZp761F241
66406	0.5706229	hypothetical protein DKFZp762E1312
51657	0.5736969	hypothetical protein ET
491465	0.5150527	hypothetical protein FLJ10035
767289	0.4432685	hypothetical protein FLJ10055

292936	0.4593712	hypothetical protein FLJ10468
753299	0.8679015	hypothetical protein FLJ10504
823907	0.4218216	hypothetical protein FLJ10511
504308	0.6041122	hypothetical protein FLJ10540
503889	0.7454098	hypothetical protein FLJ10656
40042	0.4604322	hypothetical protein FLJ10747
233349	0.762952	hypothetical protein FLJ10761
809512	0.4442565	hypothetical protein FLJ10767
246800	0.5625675	hypothetical protein FLJ10803
2052113	0.8307595	hypothetical protein FLJ10903
325515	0.4689353	hypothetical protein FLJ10980
126851	0.6559601	hypothetical protein FLJ11160
768570	0.8371438	hypothetical protein FLJ11280
266218	0.4934791	hypothetical protein FLJ11350
589232	0.7583348	hypothetical protein FLJ11506
489594	0.5308806	hypothetical protein FLJ11565
744994	0.4916322	hypothetical protein FLJ12242
743220	0.5242028	hypothetical protein FLJ12517
41569	0.7412357	hypothetical protein FLJ12650
731080	0.4979864	hypothetical protein FLJ12661
785795	0.660789	hypothetical protein FLJ12910
150003	0.77183	hypothetical protein FLJ13187
1605426	0.8909868	hypothetical protein FLJ13352
248649	0.761865	hypothetical protein FLJ13910
1554167	-1.4126653	hypothetical protein FLJ14529
1581941	0.5537015	hypothetical protein FLJ14540
259950	0.4187278	hypothetical protein FLJ14991
76196	0.4278385	hypothetical protein FLJ20062
1505038	1.2292506	hypothetical protein FLJ20171
489444	0.4741367	hypothetical protein FLJ20211
428582	0.4642013	hypothetical protein FLJ20296
2027952	0.437854	hypothetical protein FLJ20297
809507	0.4189998	hypothetical protein FLJ20568
502774	0.8091404	hypothetical protein FLJ20623
1636092	0.8997881	hypothetical protein FLJ20657
300632	-1.6969092	hypothetical protein FLJ21044 similar to Rbig1
1572710	0.4750848	hypothetical protein FLJ21213
85804	0.44449	hypothetical protein FLJ21918
429799	0.6012713	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
811907	0.5246416	hypothetical protein FLJ22056
510575	0.6040713	hypothetical protein FLJ22087
810939	0.4634658	hypothetical protein FLJ22169
2015517	0.6259564	hypothetical protein FLJ22237
1493218	-1.164886	hypothetical protein FLJ22297



1947381	0.5524634	hypothetical protein FLJ22329
37554	0.6574292	hypothetical protein FLJ22353
753378	0.6218232	hypothetical protein FLJ22649 similar to signal peptidase SPC22/23
757328	0.6097389	hypothetical protein FLJ22678
52103	0.432756	hypothetical protein FLJ23045
455275	0.4788778	hypothetical protein FLJ23469
144880	0.6332999	hypothetical protein from EUROIMAGE 1759349
1696757	0.6591801	hypothetical protein KIAA1165
625693	0.6744622	hypothetical protein MGC10911
781342	0.6159353	hypothetical protein MGC11115
1642496	0.4645092	hypothetical protein MGC11266
824879	0.8366695	hypothetical protein MGC11275
325606	0.7008219	hypothetical protein MGC14353
1898619	0.5880791	hypothetical protein MGC15737
68636	0.9562688	hypothetical protein MGC2477
490023	-1.3516302	hypothetical protein MGC2648
815501	0.4879053	hypothetical protein MGC2721
1869201	0.8202299	hypothetical protein MGC2745
1558642	0.4424721	hypothetical protein MGC2771
51773	0.7858986	hypothetical protein MGC3077
37708	0.8194577	hypothetical protein MGC3101
814443	-1.1905978	hypothetical protein MGC3232
42408	0.7559848	hypothetical protein MGC4604
123614	0.7117834	hypothetical protein MGC4675
120271	0.5626611	hypothetical protein MGC4692
120271	0.7208543	hypothetical protein MGC4692
812238	1.2132886	hypothetical protein MGC4692
1858892	0.9897362	hypothetical protein MGC4825
121251	0.6209436	hypothetical protein MGC5576
293727	0.5153298	hypothetical protein MGC861
810609	0.5036493	hypothetical protein PP1226
745606	1.3470375	hypothetical protein PP591
2028949	0.6662774	hypothetical protein PRO1855
625399	-1.0523138	hypothetical protein similar to beta-transducin family
743860	0.4189656	hypothetical protein, clone 2746033
897806	0.6470379	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
39884	0.9091807	IMP (inosine monophosphate) dehydrogenase 1
221295	0.6477514	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
788234	-1.4824055	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein



2051697	0.4197703	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
505243	-0.980381	inositol 1,4,5-triphosphate receptor, type 2
77533	0.435582	inositol polyphosphate-5-phosphatase, 40kD
207288	0.632639	insulin induced gene 1
814350	0.7701748	insulin-degrading enzyme
130201	-1.2885369	intercellular adhesion molecule 2
755599	0.6330221	interferon induced transmembrane protein 1 (9-27)
1592837	0.4355927	interferon induced transmembrane protein 2 (1-8D)
1159963	0.5133656	interferon regulatory factor 7
782513	0.5625811	interferon, alpha-inducible protein (clone IFI-6-16)
856447	0.4816395	interferon, gamma-inducible protein 30
1422723	0.4411931	interferon-induced protein 35
84295	0.4349213	interleukin 1 receptor antagonist
811920	-1.6924158	interleukin 11 receptor, alpha
1517171	0.7036866	interleukin 2 receptor, alpha
80344	-1.0323882	interleukin 7 receptor
859228	0.4942316	isocitrate dehydrogenase 1 (NADP+), soluble
869375	0.4958886	isocitrate dehydrogenase 2 (NADP+), mitochondrial
868128	0.8873517	JM4 protein
414992	0.587733	K562 cell-derived leucine-zipper-like protein 1
809784	-1.030253	kallikrein 6 (neurosin, zyme)
2243051	-0.9835274	kallikrein 8 (neuropsin/ovasin)
824962	0.595868	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
625234	0.62188	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
1474900	-1.1347123	keratin 15
1486533	0.441804	keratin 16 (focal non-epidermolytic palmoplantar keratoderma)
773922	0.7767604	KIAA0005 gene product
686172	0.7131363	KIAA0008 gene product
814054	0.958989	KIAA0040 gene product
898032	0.7852733	KIAA0097 gene product
530310	0.5686743	KIAA0143 protein
1517595	0.4409591	KIAA0175 gene product
43977	0.4309655	KIAA0182 protein
1473471	-1.2409979	KIAA0194 protein
49117	0.5274035	KIAA0215 gene product

782428	0.9524489	KIAA0250 gene product
1884404	0.6864546	KIAA0285 gene product
809944	0.7021108	KIAA0310 gene product
795805	0.5064099	KIAA0332 protein
773426	0.5941568	KIAA0391 gene product
221499	0.5317861	KIAA0508 protein
753162	-1.0416438	KIAA0603 gene product
725841	0.6051304	KIAA0662 gene product
1636166	-0.9969091	KIAA0668 protein
786265	0.5443881	KIAA0750 gene product
40173	0.7124913	KIAA0807 protein
366039	0.4701924	KIAA0892 protein
1679942	0.4215618	KIAA1053 protein
124447	0.679866	KIAA1184 protein
1640282	0.4205899	KIAA1240 protein
1518402	0.7150061	KIAA1361 protein
843054	0.5776102	KIAA1533 protein
149539	0.4671676	KIAA1700
277571	-1.2030738	KIAA1706 protein
753038	-1.1629978	kinesin family member C3
769942	0.509086	kinesin-like 4
343731	0.5365018	<b>Kruppel-like factor 2 (lung) (KLF2), Homo sapiens</b>
280249	0.6503028	Kruppel-like factor 7 (ubiquitous)
770355	0.6099761	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
767202	-1.3217103	latent transforming growth factor beta binding protein 2
897731	-0.9927981	latrophilin
199403	1.082569	lectin, galactoside-binding, soluble, 8 (galectin 8)
60565	0.720547	lethal giant larvae (Drosophila) homolog 2
470092	0.5429717	like-glycosyltransferase
2056139	-1.2697411	LIM domain protein
1469377	-1.6473741	lipoma HMGIC fusion partner-like 2
810947	0.5151346	LIS1-interacting protein NUDE1, rat homolog
825296	0.5178447	low density lipoprotein receptor defect C complementing
490778	0.6788304	low molecular mass ubiquinone-binding protein (9.5kD)
150314	0.6584621	lysophospholipase I
826363	0.6087183	lysophospholipase II
1631747	0.5245873	male-enhanced antigen
366100	-1.0467604	matrilin 2
470393	-1.2354879	matrix metalloproteinase 7 (matrilysin, uterine)
142586	0.602037	MCT-1 protein

2069602	0.4786416	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)
200814	-1.7140538	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
729975	0.9149894	meningioma expressed antigen 5 (hyaluronidase)
1518890	0.7206844	metallothionein-like 5, testis-specific (tesmin)
878406	0.6750777	metaxin 1
2014034	0.8354357	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase
124298	0.6294358	microsomal glutathione S-transferase 3
564492	0.7672548	mitochondrial carrier homolog 2
359723	0.4630712	mitochondrial elongation factor G
491524	0.5175752	mitochondrial ribosomal protein L13
2019223	0.849044	mitochondrial ribosomal protein L17
788334	0.6427785	mitochondrial ribosomal protein L23
416436	0.4252319	mitochondrial ribosomal protein L24
417801	0.5414761	mitochondrial ribosomal protein L27
782608	0.8507815	mitochondrial ribosomal protein L9
1909574	0.4342055	mitochondrial ribosomal protein S11
590774	0.8100386	mitogen-activated protein kinase 13
2326057	0.61263	MLN51 protein
1075635	0.4495618	MLSN1- and TRP-related
450301	0.4380657	mutL (E. coli) homolog 3
611443	0.6244565	myoglobin
1473274	-1.1557062	myosin regulatory light chain 2, smooth muscle isoform
629944	0.4242364	myosin VB
744944	0.5482368	myosin VI
841308	-1.200964	myosin, light polypeptide kinase
840865	0.644011	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)
1456348	0.7397574	N-acetylneuraminic acid phosphate synthase; sialic acid synthase
66599	0.4639123	N-acetyltransferase 1 (arylamine N-acetyltransferase)
1635681	0.7152705	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)
951216	0.5291832	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)
487733-2	0.5844776	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (8kD, AGGG)
487733	0.6745496	<b>NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (8kD, AGGG)</b>

753457	0.4435792	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)
611467	0.4428543	NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q reductase)
358609	0.5266332	NADH dehydrogenase (ubiquinone) flavoprotein 3 (10kD)
1762111	0.5272967	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
76605	0.9028609	nesca protein
838478	-1.5059801	neurocalcin delta
289428	-1.1923798	neurotrophic tyrosine kinase, receptor, type 2
877621	-1.3987023	nGAP-like protein
199645	0.6654138	nicastatin
811761	0.6587469	Nijmegen breakage syndrome 1 (nibrin)
825659	0.4515758	N-myc downstream regulated
75859	-2.4150177	N-myc downstream-regulated gene 2
845363	0.617901	non-metastatic cells 1, protein (NM23A) expressed in
726658	0.5157542	non-metastatic cells 3, protein expressed in
203003	0.6724027	non-metastatic cells 4, protein expressed in
795256	0.6974866	NPD007 protein
207794	0.4297389	nuclear factor (erythroid-derived 2), 45kD
416959	-1.051868	nuclear factor I/B
725649	0.4559473	nuclear factor of activated T-cells, cytoplasmic, calcineurin- dependent 4
503851	0.564048	nuclear receptor co-repressor/HDAC3 complex subunit
773188	0.6270494	nuclear receptor subfamily 1, group D, member 2
1565455	0.4634802	nuclear receptor subfamily 2, group C, member 2
377384	0.4746085	nuclear receptor subfamily 2, group F, member 2
843070	-1.1647509	nucleoporin 88kD
769890	0.4647115	nucleoside phosphorylase
773674	0.6095732	oncogene TC21
1523225	0.4511104	oncostatin M receptor
66535	0.6088919	ornithine decarboxylase antizyme 2
782608	0.7230962	<b>ornithine decarboxylase antizyme 3 (OAZ3), Homo sapiens</b>
1753497	0.5485231	ovo (Drosophila) homolog-like 1
756442	0.7115925	P450 (cytochrome) oxidoreductase
781019	0.6819736	paraoxonase 2

81203	0.4391758	paraoxonase 3
785368	0.4411742	PDZ-binding kinase; T-cell originated protein kinase
1882697	-1.3873266	peanut (Drosophila)-like 2
416676	-1.2751042	pellino (Drosophila) homolog 1
285377	-1.6514168	pellino (Drosophila) homolog 2
1587710	-1.0092611	period (Drosophila) homolog 1
1573251	0.823025	peroxisomal long-chain acyl-coA thioesterase
814353	0.4883684	phorbol-12-myristate-13-acetate-induced protein 1
897963	-1.0751021	phosphatidic acid phosphatase type 2A
346942	0.5326646	phosphatidylinositol glycan, class Q
788136	-1.0073983	phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)
625923	0.7725056	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
712401	-1.193113	phosphoinositide-3-kinase, catalytic, delta polypeptide
811142	0.4595393	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
272529	0.8371698	phosphomannomutase 2
725284	0.6014099	phosphorylase kinase, gamma 2 (testis)
1474337	-0.986117	phosphorylase, glycogen; brain
843195	0.86501	phosphoserine phosphatase
503215	0.9757636	pilin-like transcription factor
810124	0.9124035	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)
365358	0.696963	pM5 protein
290378	-1.2346086	podocalyxin-like
859761	0.8563964	poliovirus receptor-related 2 (herpesvirus entry mediator B)
744047	0.4802334	polo (Drosophila)-like kinase
897813	0.5034689	polyadenylate binding protein-interacting protein 1
741769	0.5565863	polymerase (DNA directed), beta
810734	0.6603412	polymerase (DNA-directed), delta 4
813410	0.5664086	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)
1325816	0.6742078	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)
2063982	0.4651856	potassium channel, subfamily K, member 6 (TWIK-2)
756708	-1.1346161	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4
67741	-1.4786722	PP2135 protein

69002	-1.3581187	PPAR(gamma) angiopoietin related protein
241348	0.8182422	prenylcysteine lyase
280375	0.9155003	PRO2000 protein
2020898	0.6044163	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
826173	0.4276784	profilin 1
486110	0.5127183	profilin 2
41698	0.4938629	progesterone binding protein
837864	0.4345283	progesterin induced protein
1573946	0.5875624	programmed cell death 9
138788	0.6497728	prolactin receptor
855800	0.6235647	prolyl endopeptidase
27544	-0.9834143	prominin (mouse)-like 1
810558	0.9227709	proteasome (prosome, macropain) 26S subunit, ATPase, 4
2050827	0.7156518	proteasome (prosome, macropain) 26S subunit, ATPase, 5
1553306	0.6066787	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
823598	0.9452282	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
2054635	0.831532	proteasome (prosome, macropain) subunit, alpha type, 7
122241	0.7352191	proteasome (prosome, macropain) subunit, beta type, 2
951233	0.7240615	proteasome (prosome, macropain) subunit, beta type, 3
1460110	0.6397172	proteasome (prosome, macropain) subunit, beta type, 5
1473289	0.7441483	protective protein for beta-galactosidase (galactosialidosis)
26883	0.4176151	protein kinase (cAMP-dependent, catalytic) inhibitor beta
755301	0.5790795	protein kinase C, delta
2055807	0.6216372	protein kinase domains containing protein similar to phosphoprotein C8FW
205049	0.6682666	protein kinase H11; small stress protein-like protein HSP22
756666	0.6269882	protein phosphatase 1, catalytic subunit, alpha isoform
814989	0.4419384	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
41356	0.5683316	protein phosphatase 2, regulatory subunit B (B56), alpha isoform
358162	0.616765	protein predicted by clone 23627
785707	0.5133005	protein regulator of cytokinesis 1



774502	0.4222849	protein tyrosine phosphatase, non-receptor type 12
151449	0.4189856	protein tyrosine phosphatase, non-receptor type 21
83363	0.748646	protein-L-isoaspartate (D-aspartate) O-methyltransferase
145491	0.4250102	protocadherin 1 (cadherin-like 1)
303109	-1.2557454	purinergic receptor (family A group 5)
141852	0.5762886	purinergic receptor P2Y, G-protein coupled, 2
1917941	0.9960315	purine-rich element binding protein B
744374	0.6732551	putative ankyrin-repeat containing protein
685516	0.8694652	putative G protein-coupled receptor
122077	1.2356703	putative membrane protein
261472	0.6215341	putative nuclear protein ORF1-FL49
795498	0.5557245	putative transmembrane protein
826077	0.5405591	pyruvate dehydrogenase (lipoamide) beta
365060	0.5244569	RAB11A, member RAS oncogene family
79520	0.6919579	RAB2, member RAS oncogene family
741891	0.4775456	RAB2, member RAS oncogene family-like
1911343	0.967716	RAB26, member RAS oncogene family
1639531	0.6315732	RAB27A, member RAS oncogene family
784150	0.5598483	RAB31, member RAS oncogene family
785701	0.7413837	RAB31, member RAS oncogene family
1845169	0.8033348	RAB35, member RAS oncogene family
470124	0.7539249	RAD1 (S. pombe) homolog
1476053	0.6522237	RAD51 (S. cerevisiae) homolog (E coli RecA homolog)
505864	-1.2393277	RalGDS-like gene
143426	0.5173212	ras homolog gene family, member B
45099	-1.6325981	regucalcin (senescence marker protein-30)
2106144	-1.1619925	regulated in glioma
1500542	0.5032679	regulator of G-protein signalling 11
813707	0.6252347	regulator of G-protein signalling 16
2017403	0.5117711	regulator of G-protein signalling 3
781097	0.7633668	reticulon 3
2322367	0.7249854	reticulon 4
595037	1.3057353	retinoic acid induced 3
812994	0.671102	retinoid X receptor, alpha
810959	0.505619	Rho GDP dissociation inhibitor (GDI) alpha
244801	1.0162794	Rho guanine exchange factor (GEF) 11
756373	0.4310628	Rho guanine exchange factor (GEF) 16
1422338	0.5652946	ribonucleotide reductase M2 polypeptide
990881	-1.0289558	<b>ribosomal protein L12 (Rpl12), mus musculus</b>

814316	-1.0654718	ribosomal protein L13
123441	0.7124698	ribosomal protein L7a
772898	0.520392	ribosomal protein S15a
469686	0.9203022	Ric (Drosophila)-like, expressed in many tissues
1636844	0.4627748	ring finger protein 14
133236	-1.0945253	RNA binding motif protein, X chromosome
291478	-1.3155899	runt-related transcription factor 3
756595	0.5433619	S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
810612	0.842284	S100 calcium-binding protein A11 (calgizzarin)
824108	0.4369933	SCAN domain-containing 1
416434	-1.0284229	SCN Circadian Oscillatory Protein (SCOP)
785840	0.4219115	SEC24 (S. cerevisiae) related gene family, member D
2306987	0.4670155	secreted and transmembrane 1
878836	-1.2507242	secretory granule, neuroendocrine protein 1 (7B2 protein)
840878	0.6216124	seladin-1
1492463	1.087152	selenoprotein X, 1
592801	0.4785497	serine palmitoyltransferase, long chain base subunit 2
814378	0.6857148	serine protease inhibitor, Kunitz type, 2
209066	0.7693907	serine/threonine kinase 15
209066	0.8120797	<b>serine/threonine kinase 15</b>
161456	-0.9820939	serum amyloid A1
1917449	-1.1785893	serum amyloid A4, constitutive
470061	0.9665514	seven in absentia (Drosophila) homolog 2
813631	0.5754418	seven transmembrane protein TM7SF3
49351	0.75115	SEX gene
343760	-0.9907562	SH3 domain binding glutamic acid-rich protein like 2
2302099	0.7117055	sialidase 3 (membrane sialidase)
813751	0.7659116	sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase)
785616	0.7131593	signal sequence receptor, alpha (translocon-associated protein alpha)
2504881	-1.0194516	signal transducer and activator of transcription 5A
144740	0.630134	similar to phosphatidylcholine transfer protein 2
140574	-1.2754214	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)

2322223	0.5047814	small nuclear ribonucleoprotein polypeptide A
704414	0.8520508	small nuclear ribonucleoprotein polypeptides B and B1
288999	0.9896012	small protein effector 1 of Cdc42
1692195	0.4471181	smg GDS-ASSOCIATED PROTEIN
530958	-1.0316423	smoothened (Drosophila) homolog
810762	0.5072899	SNARE protein
472103	0.503987	soc-2 (suppressor of clear, C.elegans) homolog
810875	0.4176896	solute carrier family 26, member 6
49273	0.742123	solute carrier family 27 (fatty acid transporter), member 4
782689	0.4570254	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
1702742	0.453453	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
773286	0.5158979	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1
76362	0.4553121	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
1734309	0.6672454	sperm associated antigen 4
503866	0.4884193	sperm autoantigenic protein 17
565235	0.4428854	spermine synthase
124781	0.5832065	squalene epoxidase
1558675	-1.6577507	SRY (sex determining region Y)-box 10
1469425	0.9610542	SRY (sex determining region Y)-box 22
768571	-1.1461886	SRY (sex determining region Y)-box 8
25440	0.4304195	staufen (Drosophila, RNA-binding protein) homolog 2
2018084	0.6822251	Ste-20 related kinase
302031	0.6626629	Ste20-related serine/threonine kinase
810711	0.869424	stearoyl-CoA desaturase (delta-9-desaturase)
590759	0.5791873	sterol-C4-methyl oxidase-like
35191	0.4165847	stromal cell-derived factor 2
366132	1.1911439	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD
781014	-1.2359239	suppression of tumorigenicity 5
969877	0.8382113	synaptosomal-associated protein, 25kD
177827	0.4500254	synaptotagmin VII
826194	0.5486839	synaptotagmin-like 2
135640	0.4708685	syntaxin 3A
509588	0.49319	TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD

1474955	0.8460414	TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)
726637	0.45959	t-complex-associated-testis-expressed 1-like
346696	0.5838269	TEA domain family member 4
47043	-1.0559861	tensin
795543	0.4364791	thioredoxin peroxidase (antioxidant enzyme)
965223	0.4687291	thymidine kinase 1, soluble
739126	0.6881663	tissue specific transplantation antigen P35B
825470	0.5523318	topoisomerase (DNA) II alpha (170kD)
1591264	0.5440944	transaldolase 1
347373	0.8555396	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)
823940	0.4997308	transducer of ERBB2, 1
705064	0.5238148	transforming, acidic coiled-coil containing protein 3
882248	-0.9965858	transgelin
359887	1.052326	translocase of inner mitochondrial membrane 17 (yeast) homolog A
149355	0.6943923	translocating chain-associating membrane protein
826256	0.8700831	transmembrane 7 superfamily member 1 (upregulated in kidney)
298417	0.4235025	trefoil factor 3 (intestinal)
855749	0.5432466	triosephosphate isomerase 1
740620	-1.0395569	tropomyosin 2 (beta)
611532	-1.273871	troponin I, skeletal, fast
1409509	0.7370811	troponin T1, skeletal, slow
489657	0.4609514	tryptophan rich basic protein
757489	0.5386267	tubulin, alpha 2
825585	0.6413235	tubulin-specific chaperone e
491403	-1.0411657	tumor necrosis factor receptor superfamily, member 1B
814306	0.630078	tumor protein D52
1435003	0.8098225	tumor suppressing subtransferable candidate 1
1856063	-1.0036618	tweety (Drosophila) homolog 1
292996	0.5341429	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
868396	-0.9916319	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
626318	0.4746692	ubinuclein 1
769921	0.726646	ubiquitin carrier protein E2-C

81599	0.5067033	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)
1698036	0.5843382	ubiquitin-conjugating enzyme E2 variant 1
839682	0.5542571	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
289978	0.6090234	ubiquitin-like 4
713862	0.4400704	ubiquitin-protein isopeptide ligase (E3)
824524	0.5296138	UDP-galactose transporter related
139835	0.5590106	UDP-glucose dehydrogenase
809727	0.4224266	unc-51 (C. elegans)-like kinase 1
284261	0.7445419	uncharacterized hematopoietic stem/progenitor cells protein MDS030
884498	0.5640535	uncharacterized hypothalamus protein HT012
236034	0.9534619	uncoupling protein 2 (mitochondrial, proton carrier)
783681	0.4412503	upstream regulatory element binding protein 1
769600	0.5106262	uracil-DNA glycosylase 2
81336	0.6099072	uteroglobin
1631699	0.6665952	valosin-containing protein
855563	0.5987092	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
810316	0.4245985	very long-chain acyl-CoA synthetase; lipidosin
71087	-1.2181178	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F
322617	0.5188645	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)
784140	0.6102245	WD repeat domain 15
731023	0.7151176	WD repeat domain 5
268946	0.4751692	WD40 protein Ciao1
2306221	0.4385881	wingless-type MMTV integration site family, member 10B
235986	0.5649127	wingless-type MMTV integration site family, member 11
138189	1.0692241	Wolfram syndrome 1 (wolframin)
813281	0.9107661	WW domain-containing protein 1
795185	0.9295627	xenotropic and polytropic retrovirus receptor
813629	0.7288266	YME1 (S.cerevisiae)-like 1
209537	-0.9988461	zinc finger protein 221

**Table 3** (in alphabetical order)

<b>CloneID</b>	<b>Weight</b>	<b>Description</b>
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1574058	0.6261947	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
73252	-0.6115602	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
725076	-0.6798005	5'-nucleotidase (purine), cytosolic type B
1902764	-0.5683052	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
2325804	0.5840656	95 kDa retinoblastoma protein binding protein
713782	0.5273402	a disintegrin and metalloproteinase domain 15 (metargidin)
1738208	0.7166687	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4
488505	0.4727394	accessory proteins BAP31/BAP29
1587863	0.7507482	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl- Coenzyme A thiolase)
855029	0.4904632	Ac-like transposable element
279970	0.5992634	adenosine A2a receptor
712139	-1.2371074	ADP-ribosylation factor-like 7
814798	-0.9611553	aldehyde dehydrogenase 1 family, member A3
47853	0.6077928	aldehyde dehydrogenase 4 family, member A1
196992	-0.6573113	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
23831	-0.8493217	aldolase C, fructose-bisphosphate
272706	-0.7274769	alpha2,3-sialyltransferase
1635320	-0.8845852	amiloride-sensitive cation channel 2, neuronal
809998	-0.5519459	amylase, alpha 2A; pancreatic
2250839	0.654954	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
2019101	0.4289318	angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8)
344854	-0.692296	ankyrin repeat domain 3
208718	-0.7660278	annexin A1
666879	-0.7950485	annexin A8
239568	0.5750382	annexin A9
1435862	0.8934643	antigen identified by monoclonal antibodies 12E7, F21 and O13
2110511	0.6203153	artemin
183440	0.4967506	arylsulfatase A



815737	-1.1857965	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
266312	0.6856592	ATPase, Cu <sup>++</sup> transporting, beta polypeptide (Wilson disease)
840768	0.4812559	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 16kD
810725	0.51329	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 21kD
156211	-0.8269263	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 1 (Renal tubular acidosis with deafness)
48518	-0.6455041	ATP-binding cassette, sub-family A (ABC1), member 5
813256	-0.7334866	ATP-binding cassette, sub-family B (MDR/TAP), member 1
1558108	0.5577768	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
767798	0.7682106	ATX1 (antioxidant protein 1, yeast) homolog 1
1709791	0.740832	BAI1-associated protein 1
1609665	-0.7765472	BarH-like homeobox 2
1558151	0.4723511	basic leucine zipper transcription factor, ATF-like
342181	0.557997	B-cell CLL/lymphoma 2
1456701	0.5545861	B-cell CLL/lymphoma 9
2244196	0.5432772	B-cell receptor-associated protein BAP29
1916575	0.5127478	BCL2-interacting killer (apoptosis-inducing)
809357	0.571929	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)
878798	-0.5956349	beta-2-microglobulin
786069	-0.6484842	beta-site APP-cleaving enzyme
741977	0.6758385	B-factor, properdin
1733262	0.5891897	BLu protein
293964	-0.7275302	butyrophilin, subfamily 3, member A1
271472	0.6582514	C3HC4-like zinc finger protein
1601845	-0.7178673	Ca <sup>2+</sup> -promoted Ras inactivator
773301	-0.5147295	cadherin 3, type 1, P-cadherin (placental)
841679	0.6283163	calcium and integrin binding protein (DNA-dependent protein kinase interacting protein)
772913	-0.9823487	calreticulin
359250	0.5382989	carbonic anhydrase IV
753301	-0.8393651	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)
744417	0.6563238	carnitine acetyltransferase

120106	-0.631375	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
341763	-0.5868818	caspase 5, apoptosis-related cysteine protease
72778	-0.6614808	caspase 7, apoptosis-related cysteine protease
51083	0.5170561	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)
377461	-0.7093974	caveolin 1, caveolae protein, 22kD
1946448	-0.790849	caveolin 2
1572298	-0.5126426	CD3Z antigen, zeta polypeptide (TiT3 complex)
739193	-0.7338774	cellular retinoic acid-binding protein 1
1626996	-0.5573507	c-fos induced growth factor (vascular endothelial growth factor D)
811774	0.7223819	CGI-49 protein
221846	-0.5714352	checkpoint suppressor 1
283023	-0.6577611	chemokine (C-X3-C) receptor 1
79629	-0.6849525	<b>chemokine (C-X-C motif) receptor 4 (CXCR4), Homo sapiens</b>
293569	0.8708985	chromosome 1 open reading frame 21
742562	-0.9269494	chromosome 16 open reading frame 5
1492426	0.4635224	chromosome 19 open reading frame 3
490414	-0.6078858	chromosome 2 open reading frame 2
824052	1.034408	chromosome 6 open reading frame 1
144924	-0.5498123	chromosome 6 open reading frame 5
50562	0.5195335	chromosome 8 open reading frame 4
811149	-0.5319742	chromosome 9 open reading frame 3
731308	0.6259858	citrate synthase
1656062	0.4288838	coagulation factor XII (Hageman factor)
85634	-0.5410684	complement component 1, s subcomponent
77972	-0.5144916	complement component 3
868652	0.4682053	complement component 4B
809838	0.4466933	<b>contig C013216, human</b>
127646	0.5663395	<b>contig C030249, human</b>
360778	0.4820033	<b>contig C054624, human</b>
177665	-0.5718286	<b>contig C055081, human</b>
33267	0.6679827	<b>contig C064722, human</b>
839736	-1.1019142	crystallin, alpha B
1555924	-0.9421074	CSR1 protein
488956	-0.6682156	CUG triplet repeat, RNA-binding protein 2
701751	0.6961443	cut (Drosophila)-like 1 (CCAAT displacement protein)
742595	0.6324947	cyclin-dependent kinase 5
757873	-1.0188169	cyclin-dependent kinase 5, regulatory subunit 1 (p35)

2009491	-0.5334821	cyclin-E binding protein 1
949938	0.5011384	cystatin C (amyloid angiopathy and cerebral hemorrhage)
1323448	1.3237504	cysteine-rich protein 1 (intestinal)
360254	-0.6612871	cysteine-rich, angiogenic inducer, 61
196189	0.7992668	cytochrome b-5
2013178	-1.0884449	death associated transcription factor 1
2018423	-0.6275903	death-associated protein kinase 2
756847	-0.5632582	deformed epidermal autoregulatory factor 1 (Drosophila)
296702	0.5164562	deiodinase, iodothyronine, type I
1492468	0.4643107	DEME-6 protein
563634	-0.5737239	dendritic cell protein
1161564	-0.8865787	desmuslin
705274	0.4904221	diacylglycerol kinase, delta (130kD)
760299	-0.8251086	dickkopf (Xenopus laevis) homolog 3
35828	-0.5391332	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)
742685	-0.852598	disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
767761	0.4565666	DKFZP434B168 protein
454970	-0.6853932	DKFZP434G032 protein
366353	0.9154768	DKFZP564C186 protein
770766	0.600234	DKFZP564C1940 protein
294397	0.505999	DKFZP586A0522 protein
767068	-0.6819032	DKFZP586G1517 protein
202514	0.4902228	DNA (cytosine-5-)-methyltransferase 3 alpha
263727	0.5926363	DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis)
1876217	-0.5108977	DnaJ (Hsp40) homolog, subfamily A, member 2
2018527	0.5732092	dolichyl-phosphate mannosyltransferase polypeptide 3
884462	-0.9065675	Down syndrome critical region gene 1
782688	0.4780253	dynein, axonemal, light intermediate polypeptide
1864302	-0.6943806	E74-like factor 5 (ets domain transcription factor)
840944	-0.6399619	early growth response 1
781017	-0.5676944	early growth response 2 (Krox-20 (Drosophila) homolog)
431231	-0.6692022	EGF-containing fibulin-like extracellular matrix protein 2
188335	-0.7002579	egf-like module containing, mucin-like, hormone receptor-like sequence 2

2248488	0.7033736	ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate)
74070	0.5225238	endosulfine alpha
1693357	0.4274493	endothelin 2
153760	-0.5361176	EphB1
813520	-0.5889772	EphB3
811088	-0.5445374	ephrin-B3
1577736	-1.076549	epidermal growth factor (beta-urogastrone)
504927	-0.5894078	epithelial protein up-regulated in carcinoma, membrane associated protein 17
34093	-0.5692081	EST
594500	1.158305	EST
1641894	0.5187462	EST
725321	0.44288	estrogen receptor 1
27769	-0.5501268	ESTs
34150	-0.5673709	ESTs
40027	-0.6418674	ESTs
75078	-0.7028415	ESTs
83358	0.5709886	ESTs
138672	-0.5483104	ESTs
139660	-0.79833	ESTs
162308	-0.6580605	ESTs
196435	-0.653913	ESTs
197056	-0.5440514	ESTs
281190	-0.5572026	ESTs
345032	0.4360992	ESTs
415816	-0.5750184	ESTs
462939	-0.5200097	ESTs
470148	-0.5393193	ESTs
490965	0.4389746	ESTs
544639	-0.9767278	ESTs
725622	-0.6731681	ESTs
757191	-0.5735888	ESTs
767706	0.4731085	ESTs
814209	0.6076904	ESTs
839580	0.4826315	ESTs
1031640	-0.5354869	ESTs
1257131	-0.8069059	ESTs
1517749	0.947675	ESTs
1557637	0.4588694	ESTs
1558212	-0.5458261	ESTs
1558233	0.7654043	ESTs
1577920	-0.5161377	ESTs
1880885	-0.5638973	ESTs

1883327	-0.5684295	ESTs
1909935	-0.5368632	ESTs
1911663	-0.5610314	ESTs
289760	-0.7058375	ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]
279720	0.6607182	ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.sapiens]
725978	0.5108817	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
530197	0.8206765	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
345670	-1.135654	ESTs, Moderately similar to I59348 CCAAT binding transcription factor CBF subunit C - rat [R.norvegicus]
529843	-0.7117107	ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]
289505	0.4933344	ESTs, Moderately similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]
179212	0.6499845	ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]
3172883	-0.8293392	ESTs, Weakly similar to 1709359A dopamine D4 receptor [H.sapiens]
160192	-0.5482009	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
730313	0.5887579	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
726699	0.4658249	ESTs, Weakly similar to AAB47496 NG5 [H.sapiens]
770848	-0.5188717	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
128695	0.608873	ESTs, Weakly similar to I38344 titin, cardiac muscle [H.sapiens]
344073	0.4726399	ESTs, Weakly similar to K1CI_HUMAN KERATIN, TYPE I CYTOSKELETAL 9 [H.sapiens]
950355	-0.550114	ESTs, Weakly similar to S13495 pregnancy zone protein [H.sapiens]
35147	0.6842172	ESTs, Weakly similar to unnamed protein product [H.sapiens]

488202	0.5378254	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens]
796542	-0.9052403	ets variant gene 5 (ets-related molecule)
301122	0.6041028	extracellular matrix protein 1
741139	-1.1025542	eyes absent (Drosophila) homolog 2
1469148	0.5125351	FGFR1 oncogene partner
752631	0.4426961	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
812143	0.4519186	fibronectin leucine rich transmembrane protein 3
131839	-0.959265	folate receptor 1 (adult)
628955	-0.6088522	forkhead box O1A (rhabdomyosarcoma)
796475	-0.5563457	four and a half LIM domains 3
52419	-0.6326767	Friedreich ataxia region gene X123
298122	-0.8158372	frizzled (Drosophila) homolog 7
183200	0.4955056	fumarylacetoacetate hydrolase (fumarylacetoacetase)
2016775	-0.7914834	G protein-coupled receptor, family C, group 5, member B
209137	-0.6161588	gamma-aminobutyric acid (GABA) A receptor, epsilon
183556	0.4452493	gap junction protein, alpha 4, 37kD (connexin 37)
214068	0.5357344	GATA-binding protein 3
344959	0.8945717	gene for serine/threonine protein kinase
767495	0.4922026	GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome)
1708055	0.554593	glioblastoma overexpressed
2018337	0.5163293	glucosidase, beta; acid (includes glucosylceramidase)
1609836	0.898716	glutamate-ammonia ligase (glutamine synthase)
504791	-0.6537859	glutathione S-transferase A4
344720	-0.8822302	glycophorin C (Gerbich blood group)
358217	0.6801945	glypican 4
811582	0.690137	golgi phosphoprotein 2
739578	0.5402953	GPI-anchored metastasis-associated protein homolog
132637	-0.5694152	grancalcin, EF-hand calcium-binding protein
713129	-0.5822078	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)
323238	-0.6032171	GRO1 oncogene (melanoma growth stimulating activity, alpha)
1556433	-0.7877792	GRO3 oncogene
40299	-0.78007	growth differentiation factor 10
788654	0.7336359	<b>growth factor receptor-bound protein 2</b>



788654	0.9585887	growth factor receptor-bound protein 2
810063	0.630827	growth factor, erv1 ( <i>S. cerevisiae</i> )-like (augmenter of liver regeneration)
51741	0.5094912	GTP-binding protein
767765	-0.5282008	GTP-binding protein overexpressed in skeletal muscle
308466	0.4417728	GTP-binding protein Sara
122394	0.5554851	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
360518	-0.5253745	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1
1500000	0.5871787	H2B histone family, member B
40021	-0.5240809	hairless protein (putative single zinc finger transcription factor protein, responsible for autosomal recessive universal congenital alopecia, HR gene)
1870305	-0.5558155	heat shock 27kD protein 2
471568	0.5255851	hematological and neurological expressed 1
1569187	-0.7091259	heparan sulfate (glucosamine) 3-O-sulfotransferase 4
1486082	-0.6241275	heparin-binding growth factor binding protein
488422	0.4626549	high-mobility group 20B
202577	0.5629317	histamine N-methyltransferase
611481	-0.7507264	HMG-box transcription factor TCF-3
2014373	0.8820247	HNK-1 sulfotransferase
1592715	0.4417898	Homer, neuronal immediate early gene, 3
782460	-0.5988226	Homo sapiens cDNA FLJ10500 fis, clone NT2RP2000369
171912	0.5297738	Homo sapiens cDNA FLJ10960 fis, clone PLACE1000564
854763	0.5918867	Homo sapiens cDNA FLJ11341 fis, clone PLACE1010786
825356	-0.5850287	Homo sapiens cDNA FLJ11997 fis, clone HEMBB1001458
186301	0.5537115	Homo sapiens cDNA FLJ12924 fis, clone NT2RP2004709
825327	0.4497029	Homo sapiens cDNA FLJ14105 fis, clone MAMMA1001202
503671	-1.1528584	Homo sapiens cDNA FLJ14368 fis, clone HEMBA1001122
488130	-0.5201845	Homo sapiens cDNA FLJ20767 fis, clone COL06986
241066	-0.5369493	Homo sapiens cDNA: FLJ21028 fis, clone CAE07155
823615	0.471739	Homo sapiens cDNA: FLJ21245 fis, clone COL01184

1541711	0.4694413	Homo sapiens cDNA: FLJ21513 fis, clone COL05778
131094	0.6268883	Homo sapiens cDNA: FLJ21587 fis, clone COL06946
812256	-0.5832398	Homo sapiens cDNA: FLJ21693 fis, clone COL09609
810097	-0.5423072	Homo sapiens cDNA: FLJ21721 fis, clone COLF0381
70749	-0.5295091	Homo sapiens cDNA: FLJ21874 fis, clone HEP02488
1500815	-0.6008126	Homo sapiens cDNA: FLJ22130 fis, clone HEP19632
814528	0.6329458	Homo sapiens cDNA: FLJ22139 fis, clone HEP20959
731459	0.4427978	Homo sapiens cDNA: FLJ22296 fis, clone HRC04468
753071	-1.4473398	Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
782537	0.490998	Homo sapiens cDNA: FLJ22562 fis, clone HSI01814
840266	-0.9425178	Homo sapiens cDNA: FLJ22667 fis, clone HSI08385
726703	0.5118991	Homo sapiens clone 23736 mRNA sequence
898222	0.8092364	Homo sapiens clone 24418 mRNA sequence
491519	-0.5282605	Homo sapiens clone 24775 mRNA sequence
796723	0.576028	Homo sapiens clone CDABP0014 mRNA sequence
488404	-0.6521658	Homo sapiens clone TUA8 Cri-du-chat region mRNA
752837	-0.6056177	Homo sapiens mRNA for FLJ00074 protein, partial cds
745011	-0.5836864	Homo sapiens mRNA for KIAA1750 protein, partial cds
70245	-0.6422928	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 50374
970590	-0.5383645	Homo sapiens mRNA; cDNA DKFZp434A115 (from clone DKFZp434A115)
24958	-0.5349519	Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone DKFZp434C2016)
590310	0.6299822	Homo sapiens mRNA; cDNA DKFZp434E2321 (from clone DKFZp434E2321); partial cds
137602	-0.5667198	Homo sapiens mRNA; cDNA DKFZp434G0972 (from clone DKFZp434G0972)

265103	0.702883	Homo sapiens mRNA; cDNA DKFZp547M123 (from clone DKFZp547M123)
565319	0.6603668	Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DKFZp564B1264)
813265	-0.7192289	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)
486683	-1.0075654	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)
504959	0.5953946	Homo sapiens mRNA; cDNA DKFZp586G0321 (from clone DKFZp586G0321)
22917	-0.7173328	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)
823727	0.4406546	Homo sapiens, clone IMAGE:2905978, mRNA, partial cds
782497	0.5218113	Homo sapiens, clone IMAGE:3010666, mRNA, partial cds
1631735	0.5228778	Homo sapiens, clone IMAGE:3604336, mRNA, partial cds
186768	0.6495706	Homo sapiens, clone IMAGE:3604869, mRNA
292770	0.4944242	Homo sapiens, clone IMAGE:3627860, mRNA, partial cds
1652310	0.4525789	Homo sapiens, clone MGC:19613 IMAGE:3833049, mRNA, complete cds
810002	-1.2720931	Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds
130835	0.8659688	Homo sapiens, Similar to clone FLB3816, clone IMAGE:3454380, mRNA
588262	0.5614929	Homo sapiens, Similar to RIKEN cDNA 2600001A11 gene, clone MGC:9907 IMAGE:3870073, mRNA, complete cds
1649374	0.5731982	homogentisate 1,2-dioxygenase (homogentisate oxidase)
839081	0.4939384	homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2
2017756	0.4608709	homolog of yeast MOG1
1492238	0.9155471	HSPC003 protein

178805	0.8524069	Human DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to Drosophila Scratch (Scrt), Slug and Xenopus Snail, a novel gene similar to Drosophila CG6762, STSs, GSSs and five CpG
813419	0.5602324	hydroxyacyl-Coenzyme A dehydrogenase, type II
768007	-0.547374	hypothetical protein
810402	0.4583168	hypothetical protein
811848	-0.5637994	hypothetical protein
825822	0.5134094	hypothetical protein
1734754	-0.5512835	hypothetical protein B
32489	-0.7521767	hypothetical protein DKFZp566A1524
76182	-0.6603322	hypothetical protein DKFZp761F241
725152	-0.7173869	hypothetical protein DKFZp762A227
842896	-0.8123068	hypothetical protein DKFZp762L0311
491465	0.4821169	hypothetical protein FLJ10035
503889	0.4433034	hypothetical protein FLJ10656
233349	0.6764709	hypothetical protein FLJ10761
41869	-0.7646494	hypothetical protein FLJ11017
126851	0.5535041	hypothetical protein FLJ11160
489106	0.4628623	hypothetical protein FLJ11210
768570	0.6581316	hypothetical protein FLJ11280
84464	-0.6091345	hypothetical protein FLJ12806
785733	-0.7554682	hypothetical protein FLJ12892
156363	0.5086284	hypothetical protein FLJ12934
1605426	0.5150013	hypothetical protein FLJ13352
796498	-0.5900328	hypothetical protein FLJ14007
43764	-0.6743049	hypothetical protein FLJ14033 similar to hypoxia inducible factor 3, alpha subunit
1554167	-0.7503289	hypothetical protein FLJ14529
250797	-0.7739669	hypothetical protein FLJ20038
1505038	0.43988	hypothetical protein FLJ20171
1881689	-0.568518	hypothetical protein FLJ20281
502774	0.5204735	hypothetical protein FLJ20623
1636092	0.4404649	hypothetical protein FLJ20657
810981	0.498146	hypothetical protein FLJ20699
300632	-0.8586688	hypothetical protein FLJ21044 similar to Rbig1
37671	-0.5712258	hypothetical protein FLJ21610
1636156	-0.7827089	hypothetical protein FLJ21709
1470278	-0.5449844	hypothetical protein FLJ21841
811907	0.6180993	hypothetical protein FLJ22056
767456	-0.5555493	hypothetical protein FLJ22167
1493218	-0.6292715	hypothetical protein FLJ22297

1947381	0.4311314	hypothetical protein FLJ22329
37554	0.6440792	hypothetical protein FLJ22353
1417886	-0.563564	hypothetical protein FLJ23239
220395	-0.7687195	hypothetical protein FLJ23293 similar to ARL-6 interacting protein-2
743146	0.6388187	hypothetical protein FLJ23403
509458	-0.5266016	hypothetical protein from clone 643
292388	-0.554297	<b>hypothetical protein MAC30 (MAC30), Homo sapiens</b>
1609748	0.4955206	hypothetical protein MGC10882
824879	0.5548666	hypothetical protein MGC11275
68636	0.7904354	hypothetical protein MGC2477
770869	0.4762758	hypothetical protein MGC2592
490023	-0.7621736	hypothetical protein MGC2648
1558642	0.4426424	hypothetical protein MGC2771
773142	0.4530754	hypothetical protein MGC2827
773487	-0.6598647	hypothetical protein MGC3032
37708	0.5283276	hypothetical protein MGC3101
814443	-0.5075293	hypothetical protein MGC3232
1570427	-0.601608	hypothetical protein MGC4309
42408	0.5930231	hypothetical protein MGC4604
123614	0.4800042	hypothetical protein MGC4675
120271	0.4425879	hypothetical protein MGC4692
812238	0.5237287	hypothetical protein MGC4692
1858892	0.5295858	hypothetical protein MGC4825
745606	0.8514931	hypothetical protein PP591
1704155	-0.5133015	hypothetical protein SBBI48
840677	-0.5611985	immunoglobulin kappa constant
39884	0.5659552	IMP (inosine monophosphate) dehydrogenase 1
788234	-1.0610946	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
505243	-0.5616577	inositol 1,4,5-triphosphate receptor, type 2
703964	-0.5918604	inositol polyphosphate phosphatase-like 1
180803	-0.5083354	inositol polyphosphate-1-phosphatase
32299	-0.5945347	inositol(myo)-1(or 4)-monophosphatase 2
502436	-0.5489864	insulin receptor substrate 2
814350	0.6173648	insulin-degrading enzyme
471196	-0.7192752	integral membrane protein 3
32493	-0.9043423	integrin, alpha 6
130201	-0.5468031	intercellular adhesion molecule 2
824602	-0.5965816	interferon, gamma-inducible protein 16
856447	0.494183	interferon, gamma-inducible protein 30
811920	-0.8286379	interleukin 11 receptor, alpha
1517171	0.5204242	interleukin 2 receptor, alpha
120138	0.7096046	J domain containing protein 1

414992	0.5293379	K562 cell-derived leucine-zipper-like protein 1
809784	-0.6348991	kallikrein 6 (neurosin, zyme)
1474900	-0.5693091	keratin 15
415191	-0.700303	KIAA0161 gene product
812975	-0.6527728	KIAA0172 protein
1473471	-0.7906678	KIAA0194 protein
826668	0.550158	KIAA0274 gene product
1884404	0.4878341	KIAA0285 gene product
809944	0.4291762	KIAA0310 gene product
324927	-0.5284875	KIAA0375 gene product
826622	0.5532463	KIAA0430 gene product
754028	-0.5396001	KIAA0469 gene product
753162	-0.5377767	KIAA0603 gene product
1636166	-0.7788972	KIAA0668 protein
40173	0.5771304	KIAA0807 protein
460126	-0.5652362	KIAA0819 protein
1534700	-0.8804685	KIAA0830 protein
1901310	-0.5229967	KIAA1209 protein
345056	-0.6490368	KIAA1404 protein
665384	-0.7388404	KIAA1609 protein
1881774	-0.6332545	KIAA1678
149539	0.9878366	KIAA1700
277571	-0.59335	KIAA1706 protein
703541	-0.7118124	KIAA1858 protein
278430	0.4612914	kinesin family member 5C
753038	-1.1168529	kinesin family member C3
796539	-0.803124	KRAB-associated protein 1
488025	0.8525751	Kruppel-associated box protein
132711	-0.6985643	Kruppel-like factor 5 (intestinal)
795178	-0.5532479	lactate dehydrogenase C
346545	-0.6098367	laminin, beta 1
897731	-0.6548064	latrophilin
199403	0.6027193	lectin, galactoside-binding, soluble, 8 (galectin 8)
60565	0.5192032	lethal giant larvae (Drosophila) homolog 2
470092	0.5319336	like-glycosyltransferase
712829	-0.5181236	LIM domain only 2 (rhombotin-like 1)
783698	-0.7411614	lipin 1
247616	-0.5358709	lipoma HMGIC fusion partner
1469377	-0.9086679	lipoma HMGIC fusion partner-like 2
868169	-0.6224058	lipoprotein lipase
825296	0.4858551	low density lipoprotein receptor defect C complementing
490778	0.5957445	low molecular mass ubiquinone-binding protein (9.5kD)



341759	-0.7393558	lung type-I cell membrane-associated glycoprotein
255754	0.7720883	LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein
1470048	-0.5729078	lymphocyte antigen 6 complex, locus E
341774	-0.7044768	major histocompatibility complex, class I, A
2014856	0.5837779	major histocompatibility complex, class I-like sequence
145132	0.6725186	mannose-P-dolichol utilization defect 1
589115	0.531314	matrix metalloproteinase 1 (interstitial collagenase)
470393	-0.848482	matrix metalloproteinase 7 (matrilysin, uterine)
200814	-0.7920988	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
729975	0.5908615	meningioma expressed antigen 5 (hyaluronidase)
1518890	0.4610867	metallothionein-like 5, testis-specific (tesmin)
878406	0.4311455	metaxin 1
79254	-0.541673	MHC class I region ORF
1587847	-0.5466442	minichromosome maintenance deficient (mis5, S. pombe) 6
1390584	0.4284863	mitochondrial intermediate peptidase
788334	0.6264069	mitochondrial ribosomal protein L23
417801	0.4325892	mitochondrial ribosomal protein L27
782608	0.6105794	<b>mitochondrial ribosomal protein L9</b>
782608	0.8041049	mitochondrial ribosomal protein L9
771173	0.6594128	mitochondrial ribosomal protein S21
70201	-0.7513314	mitochondrial solute carrier
590774	0.6071935	mitogen-activated protein kinase 13
2326057	0.4506179	MLN51 protein
1075635	0.4502629	MLSN1- and TRP-related
1420842	-0.5574834	mucosa associated lymphoid tissue lymphoma translocation gene 1
450301	0.8030667	mutL (E. coli) homolog 3
611443	0.6112713	myoglobin
786072	0.5450231	myosin IC
470128	-0.5652125	myosin IE
66599	0.5399379	N-acetyltransferase 1 (arylamine N-acetyltransferase)
1635681	0.5859113	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)
487733	0.4356439	<b>NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (8kD, AGGG)</b>

1762111	0.5703701	natriuretic peptide receptor C/guanylate cyclase C (atriuretic peptide receptor C)
76605	0.5482232	nesca protein
838478	-0.934433	neurocalcin delta
2306697	0.4953741	neuromedin B
289428	-0.6542789	neurotrophic tyrosine kinase, receptor, type 2
877621	-0.8289253	nGAP-like protein
306798	-0.5742664	NGFI-A binding protein 1 (EGR1 binding protein 1)
75859	-1.6337267	N-myc downstream-regulated gene 2
726658	0.5132765	non-metastatic cells 3, protein expressed in
795256	0.4753832	NPD007 protein
754040	-0.5282144	NS1-associated protein 1
416959	-0.5999728	nuclear factor I/B
753034	-0.5182019	nuclear factor I/X (CCAAT-binding transcription factor)
725649	0.4878638	nuclear factor of activated T-cells, cytoplasmic, calcineurin- dependent 4
2710524	0.6399293	nuclear receptor coactivator 3
823714	-0.7215045	nuclear receptor co-repressor/HDAC3 complex subunit
843070	-0.8071984	nucleoporin 88kD
840882	0.441569	nucleotide binding protein
42681	-0.718704	NY-REN-25 antigen
66535	0.466705	ornithine decarboxylase antizyme 2
2028722	-0.5277252	osteoblast specific factor 2 (fasciclin I-like)
781019	0.5132896	paraoxonase 2
1404774	0.5399447	parathyroid hormone-like hormone
430318	0.4681908	parvalbumin
416676	-0.8568853	pellino (Drosophila) homolog 1
285377	-0.8214706	pellino (Drosophila) homolog 2
951125	0.4675003	peroxisomal D3,D2-enoyl-CoA isomerase
788518	-0.5724497	peroxisomal membrane protein 3 (35kD, Zellweger syndrome)
289857	0.4823282	phenylethanolamine N-methyltransferase
1957136	0.5006732	phenylethanolamine N-methyltransferase
788136	-0.8998648	phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)- homolog phosphodiesterase E4)
712401	-0.5107426	phosphoinositide-3-kinase, catalytic, delta polypeptide
33949	-0.5222135	phosphoribosyl pyrophosphate synthetase-associated protein 1
1474337	-0.844539	phosphorylase, glycogen; brain
503215	0.6457259	pilin-like transcription factor

810017	0.5135433	plasminogen activator, urokinase receptor
66491	-0.5579872	plasmolipin
796904	-0.604755	pleiomorphic adenoma gene-like 1
365358	0.4756564	pM5 protein
290378	-1.0043647	podocalyxin-like
1474149	0.5138729	poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)
859761	0.5582503	poliovirus receptor-related 2 (herpesvirus entry mediator B)
741769	0.6390692	polymerase (DNA directed), beta
810734	0.5308572	polymerase (DNA-directed), delta 4
232789	0.4292025	polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)
1325816	0.6829962	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)
756708	-0.9396531	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4
1156538	0.7512287	potassium inwardly-rectifying channel, subfamily J, member 11
2017960	-0.5822336	PP1201 protein
67741	-0.7229251	PP2135 protein
69002	-0.8528453	PPAR(gamma) angiopoietin related protein
812048	-0.6438062	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)
284592	-0.9019931	PRO1659 protein
1573946	0.509585	programmed cell death 9
27544	-0.7342174	prominin (mouse)-like 1
1456118	-0.7074166	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)
1473289	0.4540707	protective protein for beta-galactosidase (galactosialidosis)
756666	0.474441	protein phosphatase 1, catalytic subunit, alpha isoform
786545	0.4453714	protein phosphatase 1, regulatory (inhibitor) subunit 3B
151449	0.5503739	protein tyrosine phosphatase, non-receptor type 21
303109	-0.6571713	purinergic receptor (family A group 5)
685516	0.5304998	putative G protein-coupled receptor
122077	0.434495	putative membrane protein
261472	0.4814013	putative nuclear protein ORF1-FL49
826077	0.503983	pyruvate dehydrogenase (lipoamide) beta
810331	0.6014164	quiescin Q6
23776	0.879215	quinoid dihydropteridine reductase

741891	0.7360507	RAB2, member RAS oncogene family-like
1911343	0.559091	RAB26, member RAS oncogene family
248886	-0.6161134	rab3 GTPase-activating protein, non-catalytic subunit (150kD)
784150	0.4763599	RAB31, member RAS oncogene family
785701	0.6496359	RAB31, member RAS oncogene family
245296	-0.5184238	RAD52 (S. cerevisiae) homolog
1686766	-0.5342051	Rag D protein
505864	-0.7020337	RalGDS-like gene
143426	0.4679928	ras homolog gene family, member B
80727	-0.5766546	receptor tyrosine kinase-like orphan receptor 1
45099	-0.5753698	regucalcin (senescence marker protein-30)
1500542	0.5341753	regulator of G-protein signalling 11
2017403	0.5568495	regulator of G-protein signalling 3
595037	0.5870709	retinoic acid induced 3
755689	-0.5122586	retinoic acid receptor, gamma
244801	0.5693836	Rho guanine exchange factor (GEF) 11
814316	-0.521831	ribosomal protein L13
51078	-0.8348835	ribosomal protein L44
133236	-0.7561129	RNA binding motif protein, X chromosome
813845	0.6018909	RNA, U transporter 1
26294	0.5137265	RNB6
291478	-1.0093382	runt-related transcription factor 3
810612	0.4352602	S100 calcium-binding protein A11 (calgizzarin)
844703	-0.5309356	Sam68-like phosphotyrosine protein, T-STAR
627248	0.4972176	SBBI31 protein
814526	-0.5156162	seb4D
378813	-0.679848	secretory leukocyte protease inhibitor (antileukoproteinase)
1492463	0.8378401	selenoprotein X, 1
207735	-0.5422739	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
531319	-0.5404527	serine/threonine kinase 12
813631	0.4607567	seven transmembrane protein TM7SF3
49351	0.4697521	SEX gene
1603583	0.4785029	SH3 domain binding glutamic acid-rich protein like
2302099	0.4967769	sialidase 3 (membrane sialidase)
345034	-0.8161772	small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)
140574	-0.8498606	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)

704414	0.5431136	small nuclear ribonucleoprotein polypeptides B and B1
288999	0.5955672	small protein effector 1 of Cdc42
530958	-0.5423532	smoothened (Drosophila) homolog
2054122	0.698129	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3
49273	0.4937997	solute carrier family 27 (fatty acid transporter), member 4
782689	0.4930071	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
815142	-0.5782827	spastic ataxia of Charlevoix-Saguenay (sacsin)
1558675	-1.4515145	SRY (sex determining region Y)-box 10
1469425	0.6055267	SRY (sex determining region Y)-box 22
768571	-0.7476813	SRY (sex determining region Y)-box 8
2018084	0.4999242	Ste-20 related kinase
302031	0.49677	Ste20-related serine/threonine kinase
366132	0.5711651	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD
22778	0.6100322	sulfortranferase family 4A, member 1
418159	-0.6038708	synaptogyrin 1
969877	0.6064355	synaptosomal-associated protein, 25kD
177827	0.5085582	synaptotagmin VII
487932	0.4419815	synaptotagmin-like 2
826194	0.6205287	synaptotagmin-like 2
346696	0.437234	TEA domain family member 4
363144	0.7924672	transcription factor AP-2 beta (activating enhancer-binding protein 2 beta)
725680	-0.6295778	transcription factor AP-2 gamma (activating enhancer-binding protein 2 gamma)
713839	-0.5088558	transcription factor AP-4 (activating enhancer-binding protein 4)
868630	-0.5426831	transforming growth factor beta-stimulated protein TSC-22
826256	0.6554059	transmembrane 7 superfamily member 1 (upregulated in kidney)
298417	0.4587501	trefoil factor 3 (intestinal)
740620	-0.5730915	tropomyosin 2 (beta)
611532	-0.5320107	troponin I, skeletal, fast
612274	-0.6108452	tubulin, alpha 1 (testis specific)
142259	-0.7380151	tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcrption factor IIIA-interacting protein
491403	-0.6760814	tumor necrosis factor receptor superfamily, member 1B



1607229	-0.7562938	tumor protein D52-like 1
1856063	-0.5866417	tweety (Drosophila) homolog 1
868396	-0.6426678	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
150897	-1.0221539	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
284261	0.6398576	uncharacterized hematopoietic stem/progenitor cells protein MDS030
236034	0.8541082	uncoupling protein 2 (mitochondrial, proton carrier)
455269	0.4761389	<b>Unknown, from Soares 1NFLS-S1</b>
769600	0.763743	uracil-DNA glycosylase 2
2072862	-0.5694163	v-akt murine thymoma viral oncogene homolog 2
810057	-0.7363941	vasoactive intestinal peptide receptor 1
855563	0.4941473	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
71087	-0.870641	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F
193913	-0.8724313	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
784140	0.4984039	WD repeat domain 15
235986	0.5371486	wingless-type MMTV integration site family, member 11
138189	0.8950816	Wolfram syndrome 1 (wolframin)
813281	0.4659334	WW domain-containing protein 1
795185	0.7765346	xenotropic and polytropic retrovirus receptor
209537	-0.7245778	zinc finger protein 221

**Table 4** (in alphabetical order)

<b>CloneID</b>	<b>Weight</b>	<b>Description</b>
770785	0.600311	1,2-alpha-mannosidase IC
1574058	0.6796357	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
430614	0.438809	2,3-bisphosphoglycerate mutase
588911	0.3427563	2',5'-oligoadenylate synthetase 1 (40-46 kD)
73252	-0.7283898	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
838366	0.5072623	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)



489755	-0.5730453	a disintegrin and metalloproteinase domain 12 (meltrin alpha)
713782	0.6149877	a disintegrin and metalloproteinase domain 15 (metargidin)
704254	0.7061648	a disintegrin and metalloproteinase domain 8
1738208	0.5240868	a disintegrin-like and metalloprotease (repolysin type) with thrombospondin type 1 motif, 4
2306682	-0.6934667	A kinase (PRKA) anchor protein (yotiao) 9
2388571	-0.5459823	A kinase (PRKA) anchor protein 8
488505	0.4981852	accessory proteins BAP31/BAP29
809894	-0.491862	acetyl-CoA synthetase
1587863	0.3980812	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
825013	-0.505654	acidic protein rich in leucines
823930	0.4800704	actin related protein 2/3 complex, subunit 1A (41 kD)
1473922	0.6450042	actin related protein 2/3 complex, subunit 3 (21 kD)
340558	0.6550804	actin related protein 2/3 complex, subunit 5 (16 kD)
726582	-0.6807781	actin-related protein 3-beta
26617	0.3371923	activated leucocyte cell adhesion molecule
265592	0.4615543	activated RNA polymerase II transcription cofactor 4
51448	-0.5031992	activating transcription factor 3
2549634	0.3692338	activator of S phase kinase
768377	0.3809674	activity-dependent neuroprotective protein
810358	-0.5403705	acyl-Coenzyme A dehydrogenase, very long chain
210862	0.4683996	acyl-Coenzyme A oxidase 1, palmitoyl
85450	0.3868399	acyl-Coenzyme A oxidase 2, branched chain
343607	0.5588222	AD-015 protein
323693	0.5047237	adaptor-related protein complex 1, sigma 1 subunit
788641	0.3638059	adaptor-related protein complex 1, sigma 2 subunit
739109	0.4986821	adaptor-related protein complex 2, sigma 1 subunit
796757	0.5122331	adaptor-related protein complex 3, sigma 1 subunit
279970	0.5502099	adenosine A2a receptor
842939	-0.5172329	adenosine deaminase, RNA-specific, B1 (homolog of rat RED1)
39600	-0.6540275	adenylate kinase 5

878815	0.3478601	ADP-ribosylation factor 3
51532	0.5758765	ADP-ribosylation factor-like 6 interacting protein
712139	-1.2738321	ADP-ribosylation factor-like 7
46248	0.640944	ADP-ribosyltransferase (NAD <sup>+</sup> ; poly (ADP-ribose) polymerase)
241489	-0.6212938	adrenergic, beta-2-, receptor, surface
774446	0.5181672	adrenomedullin
823851	-0.6182341	AE-binding protein 1
2095066	-0.676021	alcohol dehydrogenase 1C (class I), gamma polypeptide
814798	-0.9559895	aldehyde dehydrogenase 1 family, member A3
47853	0.445149	aldehyde dehydrogenase 4 family, member A1
812105	0.3731726	ALL1-fused gene from chromosome 1q
272706	-0.5914377	alpha2,3-sialyltransferase
1584628	-0.6102937	alpha-actinin-2-associated LIM protein
1635320	-0.9586226	amiloride-sensitive cation channel 2, neuronal
1605178	0.3416196	amino acid transporter system A1
248631	-0.9106505	aminomethyltransferase (glycine cleavage system protein T)
809998	-0.5144681	amylase, alpha 2A; pancreatic
809998	-0.5297152	<b>amylase, alpha 2A; pancreatic</b>
184022	-0.7070266	amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)
2250839	0.4266248	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
502753	-0.5724623	angiopoietin 2
505289	0.3595549	angiotensin II, type I receptor-associated protein
128711	0.3437491	anillin (Drosophila Scraps homolog), actin binding protein
208718	-0.9190244	annexin A1
666879	-1.0463245	annexin A8
239568	0.767277	annexin A9
1435862	0.7697423	antigen identified by monoclonal antibodies 12E7, F21 and O13
755881	-0.5473964	aquaporin 5
1568825	0.4829928	Arg/Abl-interacting protein ArgBP2
767487	0.3530592	ariadne (Drosophila) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1
824799	-0.6054867	ART-4 protein
2110511	0.5987863	artemin

50519	-0.5577761	aryl hydrocarbon receptor nuclear translocator-like
183440	0.3406314	arylsulfatase A
703707	0.4599434	aspartate beta-hydroxylase
281476	0.3210873	aspartylglucosaminidase
377275	-1.3102234	ataxia-telangiectasia group D-associated protein
712023	-0.5302372	AT-binding transcription factor 1
782439	0.3413092	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit e
815737	-0.8444322	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
825386	0.4121622	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1F0, subunit d
2018821	0.5887114	ATPase inhibitor precursor
754625	0.3503938	ATPase, Class II, type 9A
266312	0.3289707	ATPase, Cu <sup>++</sup> transporting, beta polypeptide (Wilson disease)
810725	0.7115051	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 21kD
48518	-0.4966991	ATP-binding cassette, sub-family A (ABC1), member 5
813256	-0.7731864	ATP-binding cassette, sub-family B (MDR/TAP), member 1
767798	0.560181	ATX1 (antioxidant protein 1, yeast) homolog 1
753897	0.4324066	autocrine motility factor receptor
244764	0.5450377	B7 homolog 3
796694	0.6893307	baculoviral IAP repeat-containing 5 (survivin)
1709791	0.7837549	BAI1-associated protein 1
1609665	-0.8086161	BarH-like homeobox 2
302549	0.3340582	basic transcription element binding protein 1
1898758	-0.6126872	BCE-1 protein
810552	-0.5768989	B-cell associated protein
1456701	0.6038789	B-cell CLL/lymphoma 9
1565079	0.358728	B-cell linker
2244196	0.5972111	B-cell receptor-associated protein BAP29
814899	0.4840969	BCL2/adenovirus E1B 19kD-interacting protein 3-like
2043167	0.7167431	BCL2-associated athanogene 3
1916575	0.3814206	BCL2-interacting killer (apoptosis-inducing)
1568561	0.3518952	BCL2-like 1
809357	0.5767382	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)

786069	-0.9203158	beta-site APP-cleaving enzyme
741977	0.7538359	B-factor, properdin
1420370	0.6344209	biliverdin reductase B (flavin reductase (NADPH))
1733262	0.4289711	BLu protein
811024	0.5646461	bone marrow stromal cell antigen 2
41208	-0.865227	bone morphogenetic protein 1
1616253	0.567837	breast carcinoma amplified sequence 1
191904	0.5770884	BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog
781047	0.357207	budding uninhibited by benzimidazoles 1 (yeast homolog)
588436	0.3544892	butyrate-induced transcript 1
271472	0.6978431	C3HC4-like zinc finger protein
1601845	-0.5074894	Ca <sup>2+</sup> -promoted Ras inactivator
754653	0.4405873	cadherin, EGF LAG seven-pass G-type receptor 3, flamingo (Drosophila) homolog
841679	0.7666686	calcium and integrin binding protein (DNA-dependent protein kinase interacting protein)
49630	0.3858335	calcium channel, voltage-dependent, L type, alpha 1D subunit
346134	0.4209894	calcium-regulated heat-stable protein (24kD)
772913	-0.8306579	calreticulin
144881	0.3461767	calumenin
789383	0.3341667	cAMP responsive element modulator
839796	-0.6807912	candidate tumor suppressor p33 ING1 homolog
785793	0.4367093	capping protein (actin filament) muscle Z-line, alpha 1
53039	0.3659853	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1
1660666	0.332029	carbonic anhydrase VB, mitochondrial
649084	0.4275738	carbonic anhydrase XI
1412245	0.3762847	carboxypeptidase A2 (pancreatic)
67765	0.6300886	carboxypeptidase M
753301	-0.5171758	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)
509823	0.7304507	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
744417	0.7356767	carnitine acetyltransferase
122091	0.3903482	casein kinase 2, alpha 1 polypeptide
377314	-0.561312	casein kinase 2, alpha prime polypeptide
120106	-0.5770131	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)

30170	0.3782337	caspase 3, apoptosis-related cysteine protease
341763	-0.4953701	caspase 5, apoptosis-related cysteine protease
72778	-1.1752838	caspase 7, apoptosis-related cysteine protease
1878409	-0.7869766	catechol-O-methyltransferase
774754	-0.6243946	catenin (cadherin-associated protein), beta 1 (88kD)
51083	0.5162686	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)
345538	0.4875796	cathepsin L
842994	0.6343858	cathepsin Z
377461	-1.2798035	caveolin 1, caveolae protein, 22kD
1946448	-0.7150027	caveolin 2
1572298	-0.6228686	CD3Z antigen, zeta polypeptide (TiT3 complex)
208001	-0.5640857	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)
725454	0.6669973	CDC28 protein kinase 2
683059	-0.6216483	Cdc42 effector protein 3
854645	-0.5723062	CDC-like kinase 3
786067	0.390151	cell division cycle 25B
415102	0.4387892	cell division cycle 25C
376516	0.5195127	cell division cycle 4-like
78869	0.3954821	cell membrane glycoprotein, 110000M(r) (surface antigen)
739193	-0.5457998	cellular retinoic acid-binding protein 1
2017415	0.43546	centromere protein A (17kD)
366067	0.625758	cerebellar degeneration-related protein (62kD)
1626996	-0.682449	c-fos induced growth factor (vascular endothelial growth factor D)
429222	0.3239231	CGI-107 protein
2108077	0.6312583	CGI-112 protein
726439	0.4067151	CGI-143 protein
1947647	0.4887766	CGI-147 protein
753400	0.5732322	CGI-204 protein
811774	0.9073627	CGI-49 protein
79032	0.3816428	CGI-82 protein
624667	0.5828923	CGI-92 protein
884425	0.5327862	chaperonin containing TCP1, subunit 5 (epsilon)
882484	0.5165756	chaperonin containing TCP1, subunit 7 (eta)
221846	-0.6982802	checkpoint suppressor 1

283023	-0.8413949	chemokine (C-X3-C) receptor 1
429387	0.3810004	chimerin (chimaerin) 2
770212	-0.4981295	chitinase 3-like 1 (cartilage glycoprotein-39)
72050	0.4114235	chloride channel, nucleotide-sensitive, 1A
302996	0.3698028	chloride intracellular channel 3
24729	-0.5302207	cholinergic receptor, muscarinic 1
2783721	-0.6854649	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)
2094232	0.3693257	chromosome 1 open reading frame 12
293569	0.5103638	chromosome 1 open reading frame 21
742562	-0.730047	chromosome 16 open reading frame 5
1492426	0.8445255	chromosome 19 open reading frame 3
824052	0.6375787	chromosome 6 open reading frame 1
469383	0.5558732	chromosome 8 open reading frame 1
811149	-0.9216006	chromosome 9 open reading frame 3
731308	0.5371204	citrate synthase
1634832	-0.5931096	class I cytokine receptor
124331	0.5025464	cleavage and polyadenylation specific factor 5, 25 kD subunit
815026	0.4472842	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD
510794	0.4264564	c-myc binding protein
1656062	0.4355127	coagulation factor XII (Hageman factor)
769959	-0.6720196	collagen, type IV, alpha 2
263716	-0.6767498	collagen, type VI, alpha 1
488258	-0.7574184	collagen, type XVI, alpha 1
1632252	0.404193	complement component 1, q subcomponent, alpha polypeptide
85634	-0.4961026	complement component 1, s subcomponent
77972	-0.7194713	complement component 3
898092	-0.7267434	connective tissue growth factor
230910	-0.6096107	<b>contig C004028, human</b>
1519147	-0.7548183	<b>contig C028965, human</b>
127646	0.4493747	<b>contig C030249, human</b>
823909	0.3675927	<b>contig C039966, human</b>
177665	-0.6624986	<b>contig C055081, human</b>
770992	0.3331315	<b>contig C056172, human</b>
897770	0.4270685	<b>contig C071196, human</b>
504940	-0.508056	<b>contig C075945, human</b>
108425	0.6008772	<b>contig C076797, human</b>
155806	0.3741516	<b>contigs C041196 and C066478, human</b>
119290	-0.8224756	cortic al thymocyte receptor (X. laevis CTX) like
283751	0.4567022	cortistatin



489823	0.4468978	COX17 (yeast) homolog, cytochrome c oxidase assembly protein
1416782	0.4558415	creatine kinase, brain
839736	-1.2271618	crystallin, alpha B
1555924	-0.8025163	CSR1 protein
488956	-0.70192	CUG triplet repeat, RNA-binding protein 2
701751	0.561139	cut (Drosophila)-like 1 (CCAAT displacement protein)
487444	0.3357395	cyclic AMP phosphoprotein, 19 kD
2308346	-0.5268833	cyclin-dependent kinase 2
742595	0.6265846	cyclin-dependent kinase 5
757873	-0.6940266	cyclin-dependent kinase 5, regulatory subunit 1 (p35)
700792	0.4949149	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
1323448	1.397391	cysteine-rich protein 1 (intestinal)
360254	-0.9286811	cysteine-rich, angiogenic inducer, 61
796984	-0.5010588	cytochrome b-245, beta polypeptide (chronic granulomatous disease)
196189	0.5916252	cytochrome b-5
1455394	0.3811391	cytochrome c
278531	0.4663008	cytochrome c oxidase subunit VIc
1601947	0.6045149	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
884511	0.3440809	cytochrome c oxidase subunit VIIb
38356	0.4513099	cytochrome P450, subfamily 46 (cholesterol 24-hydroxylase)
768064	0.673441	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1
724888	0.3272422	cytochrome P450, subfamily IVB, polypeptide 1
162775	-0.5385174	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD)
2018423	-0.501705	death-associated protein kinase 2
810039	0.3662086	defender against cell death 1
296702	0.4670993	deiodinase, iodothyronine, type I
1492468	0.4878466	DEME-6 protein
810156	0.4561539	deoxythymidylate kinase (thymidylate kinase)
1161564	-1.3891189	desmuslin
842980	0.6081528	developmentally regulated GTP-binding protein 1
415613	-0.5528761	DHHC1 protein
795401	0.3573481	diacylglycerol O-acyltransferase (mouse) homolog
813387	0.4727653	diaphorase (NADH/NADPH) (cytochrome b-5 reductase)

760299	-1.7010462	dickkopf (Xenopus laevis) homolog 3
35828	-0.7163689	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)
742685	-1.272916	disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
767761	0.4608709	DKFZP434B168 protein
810998	0.3179036	DKFZP434C131 protein
825740	0.5762093	DKFZp434J1813 protein
366353	0.6203012	DKFZP564C186 protein
770766	0.4603527	DKFZP564C1940 protein
593840	-0.5033966	DKFZP564K1964 protein
345423	0.4694596	DKFZP564M112 protein
1635062	-0.8243024	DKFZP586A011 protein
294397	0.3744208	DKFZP586A0522 protein
2011515	0.5566484	DKFZP586B0923 protein
825282	0.3624112	DKFZP586L0724 protein
1909433	-0.5638242	DKFZP727C091 protein
202514	0.5045411	DNA (cytosine-5-)-methyltransferase 3 alpha
276915	0.3851081	DNA (cytosine-5-)-methyltransferase 3 beta
809466	0.3568464	DNA segment on chromosome 19 (unique) 1177 expressed sequence
754046	0.3464097	DNA segment on chromosome X (unique) 9879 expressed sequence
263727	0.4767486	DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis)
454896	0.5013449	DnaJ (Hsp40) homolog, subfamily A, member 2
1637302	0.3353374	DNAJ domain-containing
2018527	0.4717524	dolichyl-phosphate mannosyltransferase polypeptide 3
884462	-0.8743987	Down syndrome critical region gene 1
154610	0.4410751	dynactin 4
593023	-0.7516846	dystrobrevin, beta
1864302	-0.6932327	E74-like factor 5 (ets domain transcription factor)
840944	-0.7099353	early growth response 1
781017	-0.8526926	early growth response 2 (Krox-20 (Drosophila) homolog)
431231	-0.7182897	EGF-containing fibulin-like extracellular matrix protein 2
188335	-0.7399294	egf-like module containing, mucin-like, hormone receptor-like sequence 2
295986	0.413087	emopamil-binding protein (sterol isomerase)

2248488	0.4645687	ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate).
823574	0.457224	endosulfine alpha
66532	-0.5773248	endothelin 3
122147	0.5067128	<b>engulfment and cell motility 2 (ced-12 homolog, C. elegans) (ELMO2), Homo sapiens</b>
2252954	-0.6687686	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related)
366834	0.3217743	envoplakin
153760	-0.9227865	EphB1
813520	-0.7092422	EphB3
1474684	0.3291536	ephrin-A1
811088	-1.0851546	ephrin-B3
1577736	-0.6215965	epidermal growth factor (beta-urogastrone)
109863	0.559767	epithelial membrane protein 2
785967	-0.6049171	erythrocyte membrane protein band 4.1-like 2
34093	-0.8800259	EST
208969	-0.561267	EST
594500	0.5474088	EST
1623016	-0.6263561	EST
1641894	0.4277815	EST
358267	0.4719017	EST, Moderately similar to AF119917 63 PRO2831 [H.sapiens]
415415	-0.646492	EST, Moderately similar to RL1X_HUMAN 60S RIBOSOMAL PROTEIN L18A [H.sapiens]
27769	-0.8298821	ESTs
34150	-0.7263513	ESTs
40027	-0.7779473	ESTs
41826	0.4456463	ESTs
43679	-0.5063146	ESTs
46716	0.3557556	ESTs
53081	-0.5446617	ESTs
70606	0.481356	ESTs
75078	-0.6362307	ESTs
81316	-0.6176265	ESTs
83358	0.4380365	ESTs
134192	-0.4908497	ESTs
134918	0.3779855	ESTs
139660	-0.7677153	ESTs
140635	0.4706227	ESTs
160609	-0.8405669	ESTs
162308	-0.7654139	<b>ESTs</b>
162308	-0.8910356	ESTs
196435	-0.9665947	ESTs

197056	-0.5128128	ESTs
214996	0.380548	ESTs
250313	0.4121296	ESTs
266500	0.3758559	ESTs
281190	-0.7927001	ESTs
290101	0.4071477	ESTs
298143	0.3307258	ESTs
300099	0.3547857	ESTs
344091	0.4871044	ESTs
365738	0.6740773	ESTs
415816	-0.8887425	ESTs
462939	-0.5662456	ESTs
470148	-0.712917	ESTs
544639	-0.8275232	ESTs
564847	0.573202	ESTs
564981	0.4782207	ESTs
725622	-0.5370309	ESTs
754628	0.7195265	ESTs
757191	-0.8247438	ESTs
782547	0.3708058	ESTs
784105	0.5259815	ESTs
812161	-0.4948424	ESTs
814209	0.4602081	ESTs
814826	-0.8443265	ESTs
827171	0.7154964	ESTs
839580	0.3216628	ESTs
1027283	0.3242547	ESTs
1257131	-0.8163443	ESTs
1466893	-0.6364598	ESTs
1500162	0.6416738	ESTs
1517749	0.5045134	ESTs
1522734	-0.5618289	ESTs
1534493	-0.5376323	ESTs
1536006	0.5590182	ESTs
1537001	0.59528	ESTs
1557637	0.3805285	ESTs
1558233	0.4622449	ESTs
1577920	-0.5496944	ESTs
1585492	0.3812472	ESTs
1637829	0.3246232	ESTs
1700436	0.5569949	ESTs
1707637	-0.5964339	ESTs
1712825	-0.6204409	ESTs
1899312	0.3551595	ESTs
1909935	-0.8169271	ESTs

1911663	-0.5168962	ESTs
2046679	0.3358043	ESTs
431505	0.5670119	ESTs, Highly similar to A31026 probable membrane receptor protein [H.sapiens]
279633	0.3907503	ESTs, Highly similar to I38759 zinc finger/leucine zipper protein [H.sapiens]
289760	-1.1390686	ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]
345023	-0.5166203	ESTs, Highly similar to T08701 hypothetical protein DKFZp564N123.1 [H.sapiens]
322024	-0.5714933	ESTs, Highly similar to T12495 hypothetical protein DKFZp434H071.1 [H.sapiens]
46129	-0.6919169	ESTs, Highly similar to T17245 hypothetical protein DKFZp586J0917.1 [H.sapiens]
79726	0.4162264	ESTs, Highly similar to T46395 hypothetical protein DKFZp434I1120.1 [H.sapiens]
279720	0.3282308	ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.sapiens]
725978	0.5147267	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
530197	0.6122721	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
593431	0.5235073	ESTs, Moderately similar to CEGT_HUMAN CERAMIDE GLUCOSYLTRANSFERASE [H.sapiens]
345670	-1.4445337	ESTs, Moderately similar to I59348 CCAAT binding transcription factor CBF subunit C - rat [R.norvegicus]
529843	-1.0036824	ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]
120749	0.5060444	ESTs, Moderately similar to KIAA1215 protein [H.sapiens]
283124	-0.7933772	ESTs, Moderately similar to LONG-CHAIN FATTY ACID TRANSPORT PROTEIN [M.musculus]
138242	-0.5621088	ESTs, Moderately similar to MAS2_HUMAN MANNAN-BINDING LECTIN SERINE PROTEASE 2 PRECURSOR [H.sapiens]

289505	0.3714361	ESTs, Moderately similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]
179212	0.3649976	ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]
1926246	-0.701769	ESTs, Moderately similar to T46371 hypothetical protein DKFZp434P1018.1 [H.sapiens]
160192	-1.1751869	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
2017721	0.3781067	ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]
810497	0.3367408	ESTs, Weakly similar to A35363 synapsin I splice form a [H.sapiens]
73009	0.4822587	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
726699	0.3695061	ESTs, Weakly similar to AAB47496 NG5 [H.sapiens]
746163	0.5009715	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
770848	-0.5767154	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
346902	-0.5794362	ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
2016908	0.8282806	ESTs, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens]
488642	0.4881613	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
128695	0.3455381	ESTs, Weakly similar to I38344 titin, cardiac muscle [H.sapiens]
1640821	0.7790286	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
841621	0.4020253	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
742707	0.6476434	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens]
767164	-0.842198	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens]
2029173	0.8213721	ESTs, Weakly similar to N-WASP [H.sapiens]



753745	-0.4917192	ESTs, Weakly similar to S57447 HPBR11-7 protein [H.sapiens]
1583198	0.39981	ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]
1897944	-0.4855156	ESTs, Weakly similar to T00366 hypothetical protein KIAA0669 [H.sapiens]
2572170	0.4277651	ESTs, Weakly similar to T26581 hypothetical protein Y32B12A.3 - Caenorhabditis elegans [C.elegans]
358936	0.4314082	ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]
743589	0.568516	ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]
35147	1.0886084	ESTs, Weakly similar to unnamed protein product [H.sapiens]
1910078	0.3491481	ESTs, Weakly similar to YK54_YEAST HYPOTHETICAL 18.4 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [S.cerevisiae]
488202	0.8463961	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens]
414999	-0.5002542	ets variant gene 4 (E1A enhancer-binding protein, E1AF)
796542	-1.2625621	ets variant gene 5 (ets-related molecule)
1590021	-0.5302114	ets variant gene 6 (TEL oncogene)
299720	-0.5284407	<b>eukaryotic translation elongation factor 1 alpha 1</b>
299720	-0.5378801	eukaryotic translation elongation factor 1 alpha 1
299720	-0.5388238	eukaryotic translation elongation factor 1 alpha 1
299720	-0.5565137	<b>eukaryotic translation elongation factor 1 alpha 1</b>
811837	-0.848137	<b>eukaryotic translation elongation factor 1 alpha 1</b>
811837	-0.8764231	eukaryotic translation elongation factor 1 alpha 1
469151	0.4462659	eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD )
824479	0.3225263	exonuclease NEF-sp
74566	0.3226444	exportin 1 (CRM1, yeast, homolog)
301122	0.5368073	extracellular matrix protein 1
741139	-0.8299902	eyes absent (Drosophila) homolog 2
782503	0.4334388	fatty acid desaturase 1
1758590	0.6040962	fatty-acid-Coenzyme A ligase, long-chain 3
858167	-0.6453859	fatty-acid-Coenzyme A ligase, long-chain 4
1469148	0.3776558	FGFR1 oncogene partner

855755	-0.4897236	fibrillarin
154472	-0.6253276	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)
752631	0.650399	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
789012	0.6104002	fibulin 2
1570663	0.3656056	FK506-binding protein 4 (59kD)
813616	0.3608471	FK506-binding protein like
376875	0.490328	flavin containing monooxygenase 1
131839	-1.2372478	folate receptor 1 (adult)
772220	0.4352917	for protein disulfide isomerase-related
628955	-0.8761473	forkhead box O1A (rhabdomyosarcoma)
796475	-0.8041136	four and a half LIM domains 3
52419	-1.0368509	Friedreich ataxia region gene X123
298134	-0.6152731	frizzled (Drosophila) homolog 1
2309073	0.5226599	frizzled (Drosophila) homolog 5
298122	-1.1962478	frizzled (Drosophila) homolog 7
140071	-0.5708303	frizzled-related protein
1499828	0.4030396	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)
183200	0.4697062	fumarylacetoacetate hydrolase (fumarylacetoacetase)
204686	0.4687565	FXYP domain-containing ion transport regulator 1 (phospholemman)
2016775	-0.8063264	G protein-coupled receptor, family C, group 5, member B
842825	0.5047729	G1 to S phase transition 1
81409	-0.6338327	GABA(A) receptor-associated protein like 1
469306	-0.5113377	gastrin-releasing peptide
214068	0.3414185	GATA-binding protein 3
1393018	0.5404243	general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD )
2016194	0.4417536	glia maturation factor, beta
1708055	0.3225042	glioblastoma overexpressed
741474	0.7732047	glucose phosphate isomerase
2018337	0.4833207	glucosidase, beta; acid (includes glucosylceramidase)
1609836	1.0164283	glutamate-ammonia ligase (glutamine synthase)
868400	-0.4928479	glutaminyI-tRNA synthetase
731044	0.8169506	glutaredoxin 2
1848977	0.5015371	glycerol kinase
344720	-1.5196431	glycophorin C (Gerbich blood group)
491001	0.3884144	glyoxalase I

358217	0.4385343	glypican 4
686552	0.7231319	golgi phosphoprotein 1
811582	0.3319191	golgi phosphoprotein 2
431805	0.405447	granulin
323238	-0.7042807	GRO1 oncogene (melanoma growth stimulating activity, alpha)
1556433	-1.1222978	GRO3 oncogene
752643	0.5732323	group XII secreted phospholipase A2
796181	-0.8888496	growth arrest-specific 6
131268	0.3564734	growth factor receptor-bound protein 14
788654	0.6866898	<b>growth factor receptor-bound protein 2</b>
788654	1.2615322	growth factor receptor-bound protein 2
810063	0.620086	growth factor, erv1 ( <i>S. cerevisiae</i> )-like (augmenter of liver regeneration)
51741	0.4678807	GTP-binding protein
767765	-0.7691523	GTP-binding protein overexpressed in skeletal muscle
308466	0.6800103	GTP-binding protein Sara
292213	0.4014458	guanine nucleotide binding protein (G protein), beta polypeptide 2
190059	-0.634814	guanine nucleotide binding protein (G protein), gamma 7
1032831	-0.5764161	glycosyltransferase
1711456	-0.4896574	H factor (complement)-like 1
66317	0.4132405	H1 histone family, member 2
283919	0.937383	H2A histone family, member L
488964	0.9569176	H2A histone family, member O
290841	0.8346933	H2B histone family, member A
1500000	1.0118809	H2B histone family, member B
430235	0.5874504	H2B histone family, member Q
815781	0.4441245	heat shock 105kD
1870305	-0.6958213	heat shock 27kD protein 2
471568	0.8264546	hematological and neurological expressed 1
1569187	-1.2971252	heparan sulfate (glucosamine) 3-O-sulfotransferase 4
1486082	-0.6635259	heparin-binding growth factor binding protein
770845	0.5870877	hexokinase 1
1637282	0.4777562	hexokinase 2
345787	0.4647372	highly expressed in cancer, rich in leucine heptad repeats
172517	0.5869599	hippocalcin-like 1
2116188	-0.5046972	histone deacetylase 5
1434948	0.3849593	HIV TAT specific factor 1
325365	-0.7012106	HIV-1 rev binding protein 2
611481	-0.6894079	HMG-box transcription factor TCF-3

1434905	0.3624537	homeo box B7
347726	0.377767	homeo box D8
1592715	0.4944665	Homer, neuronal immediate early gene, 3
669379	0.4011648	Homo sapiens BAC clone RP11-505D17 from 7p22-p21
486179	-0.5443525	Homo sapiens cDNA FLJ10205 fis, clone HEMBA1004954
742581	0.440367	Homo sapiens cDNA FLJ10366 fis, clone NT2RM2001420
323780	-0.8879854	Homo sapiens cDNA FLJ11177 fis, clone PLACE1007402
796152	-0.6356106	Homo sapiens cDNA FLJ11685 fis, clone HEMBA1004934
825356	-0.533771	Homo sapiens cDNA FLJ11997 fis, clone HEMBB1001458
1474424	0.5021308	Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328
308539	-0.6726187	Homo sapiens cDNA FLJ12777 fis, clone NT2RP2001720
566443	0.3705134	Homo sapiens cDNA FLJ12793 fis, clone NT2RP2002033
212542	0.5587394	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321
270826	-0.9389651	Homo sapiens cDNA FLJ13329 fis, clone OVARC1001795
681992	-0.7691299	Homo sapiens cDNA FLJ13384 fis, clone PLACE1001062, highly similar to Homo sapiens mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase
647866	0.3706822	Homo sapiens cDNA FLJ13975 fis, clone Y79AA1001585
283739	0.3714571	Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838
366156	0.3861394	Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838
487831	0.3464379	Homo sapiens cDNA FLJ14059 fis, clone HEMBB1000573
825327	0.6094796	Homo sapiens cDNA FLJ14105 fis, clone MAMMA1001202
35626	0.39822	Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955
503671	-0.5461871	Homo sapiens cDNA FLJ14368 fis, clone HEMBA1001122
594226	0.403676	Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409
1492780	0.6544659	Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409
488130	-0.5289721	Homo sapiens cDNA FLJ20767 fis, clone COL06986

823615	0.3462131	Homo sapiens cDNA: FLJ21245 fis, clone COL01184
770675	0.454729	Homo sapiens cDNA: FLJ21323 fis, clone COL02374
564801	-0.5824549	Homo sapiens cDNA: FLJ21409 fis, clone COL03924
131094	0.8675719	Homo sapiens cDNA: FLJ21587 fis, clone COL06946
810097	-0.5487174	Homo sapiens cDNA: FLJ21721 fis, clone COLF0381
220293	-0.5078291	Homo sapiens cDNA: FLJ21800 fis, clone HEP00618
1500815	-0.4934665	Homo sapiens cDNA: FLJ22130 fis, clone HEP19632
814528	0.6878182	Homo sapiens cDNA: FLJ22139 fis, clone HEP20959
68534	-0.5724394	Homo sapiens cDNA: FLJ22290 fis, clone HRC04405
753071	-1.2529315	Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
840266	-1.1476896	Homo sapiens cDNA: FLJ22667 fis, clone HSI08385
491186	-0.5507413	Homo sapiens cDNA: FLJ23131 fis, clone LNG08502
745394	0.4147627	Homo sapiens cDNA: FLJ23249 fis, clone COL04196
2017917	0.360911	Homo sapiens cDNA: FLJ23371 fis, clone HEP16068, highly similar to HSTFIISH Homo sapiens mRNA for transcription elongation factor TFIIIS
727078	0.6263882	Homo sapiens cDNA: FLJ23602 fis, clone LNG15735
823694	0.4280476	Homo sapiens chromosome 19, BAC CIT-HSPC_204F22 (BC228680), complete sequence; contains bacterial insertion element
491519	-0.561401	Homo sapiens clone 24775 mRNA sequence
78736	0.3354693	Homo sapiens clone 24877 mRNA sequence
649977	0.3534567	Homo sapiens clone CDABP0014 mRNA sequence
796723	0.8573155	Homo sapiens clone CDABP0014 mRNA sequence
502689	-0.6739476	Homo sapiens clone HH409 unknown mRNA
415589	0.3296266	Homo sapiens clone PP1498 unknown mRNA
855406	0.3241172	Homo sapiens clone TCCCIA00176 mRNA sequence

488404	-0.9880176	Homo sapiens clone TUA8 Cri-du-chat region mRNA
768452	0.6018854	Homo sapiens EST from clone 491476, full insert
752837	-0.5794612	Homo sapiens mRNA for FLJ00074 protein, partial cds
2028916	0.3516982	Homo sapiens mRNA for Hmob33 protein, 3' untranslated region
282404	-0.5528532	Homo sapiens mRNA for KIAA1671 protein, partial cds
743977	0.4368155	Homo sapiens mRNA for TL132
1968422	-0.5802058	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1968422
327506	0.4152106	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 327506
70245	-0.795375	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 50374
970590	-0.8333968	Homo sapiens mRNA; cDNA DKFZp434A115 (from clone DKFZp434A115)
119133	0.3564449	Homo sapiens mRNA; cDNA DKFZp434B231 (from clone DKFZp434B231)
44292	0.6122043	Homo sapiens mRNA; cDNA DKFZp434C107 (from clone DKFZp434C107)
1871116	-0.9821709	Homo sapiens mRNA; cDNA DKFZp434C1714 (from clone DKFZp434C1714); partial cds
24958	-0.7225195	Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone DKFZp434C2016)
1883028	0.3345488	Homo sapiens mRNA; cDNA DKFZp434J1912 (from clone DKFZp434J1912)
754157	-0.7165332	Homo sapiens mRNA; cDNA DKFZp434K2172 (from clone DKFZp434K2172)
2016648	0.7633048	Homo sapiens mRNA; cDNA DKFZp434N1728 (from clone DKFZp434N1728)
785538	-0.6289951	Homo sapiens mRNA; cDNA DKFZp434N2116 (from clone DKFZp434N2116)
265103	0.5361177	Homo sapiens mRNA; cDNA DKFZp547M123 (from clone DKFZp547M123)
565319	1.0969429	Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DKFZp564B1264)



813265	-1.2230435	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)
486683	-1.2614406	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)
1844765	0.57783	Homo sapiens mRNA; cDNA DKFZp564O1763 (from clone DKFZp564O1763)
67067	-0.6003961	Homo sapiens mRNA; cDNA DKFZp564O222 (from clone DKFZp564O222)
490668	-0.7364434	Homo sapiens mRNA; cDNA DKFZp586B211 (from clone DKFZp586B211)
754192	0.3225824	Homo sapiens mRNA; cDNA DKFZp586H0924 (from clone DKFZp586H0924)
1461477	0.5343834	Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324)
1584540	-0.9754693	Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022)
595637	-0.5373697	Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012)
132857	-1.0084069	Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone DKFZp586N1323)
744918	-0.6552361	Homo sapiens mRNA; cDNA DKFZp761I0911 (from clone DKFZp761I0911)
22917	-1.1590598	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)
343079	-0.5224833	Homo sapiens mRNA; cDNA DKFZp761P0114 (from clone DKFZp761P0114)
78946	-0.648366	Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence
74738	0.409593	Homo sapiens, clone IMAGE:3535294, mRNA, partial cds
1519013	0.3628651	Homo sapiens, clone IMAGE:3537447, mRNA, partial cds
1631735	0.5502891	Homo sapiens, clone IMAGE:3604336, mRNA, partial cds
186768	0.6550741	Homo sapiens, clone IMAGE:3604869, mRNA

292770	0.6231261	Homo sapiens, clone IMAGE:3627860, mRNA, partial cds
767982	-0.533231	Homo sapiens, clone IMAGE:4134852, mRNA, partial cds
183704	-0.5184644	Homo sapiens, clone MGC:13446 IMAGE:4275731, mRNA, complete cds
241677	0.3332521	Homo sapiens, clone MGC:18110 IMAGE:4152745, mRNA, complete cds
1652310	0.4321289	Homo sapiens, clone MGC:19613 IMAGE:3833049, mRNA, complete cds
810002	-1.3038896	Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds
810567	0.3243984	Homo sapiens, clone MGC:3182 IMAGE:3356293, mRNA, complete cds
288748	-0.5493871	Homo sapiens, clone MGC:5352 IMAGE:3048106, mRNA, complete cds
50892	-0.6887497	Homo sapiens, clone MGC:9913 IMAGE:3870821, mRNA, complete cds
1635665	0.430087	Homo sapiens, RIKEN cDNA 2010100O12 gene, clone MGC:14813 IMAGE:4133274, mRNA, complete cds
491527	0.4219324	Homo sapiens, Similar to CG7083 gene product, clone MGC:10534 IMAGE:3957147, mRNA, complete cds
130835	0.3209345	Homo sapiens, Similar to clone FLB3816, clone IMAGE:3454380, mRNA
306806	0.324179	Homo sapiens, Similar to hypothetical protein FLJ12838, clone IMAGE:4130879, mRNA, partial cds
41123	0.3739475	Homo sapiens, Similar to RIKEN cDNA 2210021G21 gene, clone MGC:14859 IMAGE:3621871, mRNA, complete cds
242706	0.3562469	Homo sapiens, Similar to RIKEN cDNA 5730494N06 gene, clone MGC:13349 IMAGE:4249231, mRNA, complete cds
839746	0.4699443	Homo sapiens, Similar to RIKEN cDNA 5830420C20 gene, clone IMAGE:3633379, mRNA, partial cds
1649374	0.3771383	homogentisate 1,2-dioxygenase (homogentisate oxidase)
1492238	0.9019233	HSPC003 protein
796469	1.0269115	HSPC150 protein similar to ubiquitin-conjugating enzyme
772925	0.5562164	HSPCO34 protein
470099	0.6915952	HT002 protein; hypertension-related calcium-regulated gene
253884	-0.4897811	Human BAC clone GS1-99H8
241043	0.3770901	Human clone 137308 mRNA, partial cds

83999	-0.5044612	Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat prote
178805	1.0274897	Human DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to Drosophila Scratch (Scrt), Slug and Xenopus Snail, a novel gene similar to Drosophila CG6762, STSs, GSSs and five CpG
277627	-0.5329107	Human SH3 domain-containing protein SH3P18 mRNA, complete cds
811585	0.5288102	huntingtin (Huntington disease)
1554549	0.9764206	hydroxyacyl glutathione hydrolase
813419	0.5447006	hydroxyacyl-Coenzyme A dehydrogenase, type II
256619	0.6102239	hydroxysteroid (17-beta) dehydrogenase 7
810728	-0.7607171	hypothetical gene ZD52F10
80764	0.5510626	hypothetical protein
139354	0.4582974	hypothetical protein
140289	0.4624364	hypothetical protein
595213	0.4824381	hypothetical protein
768007	-0.5983563	hypothetical protein
785766	0.5731938	hypothetical protein
810402	0.5555749	hypothetical protein
811848	-1.1350073	hypothetical protein
824943	0.3527414	hypothetical protein
825822	0.4255725	hypothetical protein
841260	0.3801713	hypothetical protein
2271240	-0.5782432	hypothetical protein
299815	0.4482635	hypothetical protein DC42
150118	0.4039789	hypothetical protein DKFZp434F054
32489	-0.7571259	hypothetical protein DKFZp566A1524
489351	0.7003616	hypothetical protein DKFZp566J2046
746190	0.4430243	hypothetical protein DKFZp761B1514
76182	-0.9106484	hypothetical protein DKFZp761F241
725152	-0.6591675	hypothetical protein DKFZp762A227
66406	0.5966701	hypothetical protein DKFZp762E1312
842896	-0.5137089	hypothetical protein DKFZp762L0311
51657	0.4208387	hypothetical protein ET
491465	0.5420241	hypothetical protein FLJ10035
767289	0.4323485	hypothetical protein FLJ10055
172783	-0.6088873	hypothetical protein FLJ10390

292936	0.4217115	hypothetical protein FLJ10468
753299	0.6694573	hypothetical protein FLJ10504
823907	0.4135955	hypothetical protein FLJ10511
504308	0.5564295	hypothetical protein FLJ10540
131012	-0.4897744	hypothetical protein FLJ10633
503889	0.5930018	hypothetical protein FLJ10656
40042	0.3362557	hypothetical protein FLJ10747
233349	0.5446353	hypothetical protein FLJ10761
246800	0.4927231	hypothetical protein FLJ10803
343695	-0.7706809	hypothetical protein FLJ10875
2052113	0.7627076	hypothetical protein FLJ10903
325515	0.444486	hypothetical protein FLJ10980
41869	-0.6747514	hypothetical protein FLJ11017
126851	0.5454014	hypothetical protein FLJ11160
503335	-0.6944661	hypothetical protein FLJ11196
768570	0.7102463	hypothetical protein FLJ11280
266218	0.4362517	hypothetical protein FLJ11350
589232	0.6551447	hypothetical protein FLJ11506
489594	0.5178551	hypothetical protein FLJ11565
744994	0.3526118	hypothetical protein FLJ12242
743220	0.3566593	hypothetical protein FLJ12517
41569	0.4974126	hypothetical protein FLJ12650
731080	0.4276128	hypothetical protein FLJ12661
84464	-0.5426397	hypothetical protein FLJ12806
785733	-0.6476493	hypothetical protein FLJ12892
785795	0.598504	hypothetical protein FLJ12910
530036	-0.6324794	hypothetical protein FLJ13078
150003	0.8251408	hypothetical protein FLJ13187
810411	0.400096	hypothetical protein FLJ13222
1605426	0.787298	hypothetical protein FLJ13352
770935	-0.8700104	hypothetical protein FLJ13511
248649	0.5975539	hypothetical protein FLJ13910
1554167	-1.0818834	hypothetical protein FLJ14529
1581941	0.5676045	hypothetical protein FLJ14540
1636360	-0.5629882	hypothetical protein FLJ14957
259950	0.364359	hypothetical protein FLJ14991
250797	-0.6124667	hypothetical protein FLJ20038
76196	0.3781541	hypothetical protein FLJ20062
1505038	1.1904802	hypothetical protein FLJ20171
52724	-0.6199204	hypothetical protein FLJ20241
428582	0.4684705	hypothetical protein FLJ20296
2027952	0.3307056	hypothetical protein FLJ20297
753320	0.4744893	hypothetical protein FLJ20533
745490	-0.6329354	hypothetical protein FLJ20607
502774	0.7148695	hypothetical protein FLJ20623

1636092	0.7270017	hypothetical protein FLJ20657
300632	-1.2368481	hypothetical protein FLJ21044 similar to Rbig1
1572710	0.3725734	hypothetical protein FLJ21213
1470278	-0.6633411	hypothetical protein FLJ21841
85804	0.4171445	hypothetical protein FLJ21918
429799	0.6915155	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
1636669	0.4384707	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
811907	0.4340842	hypothetical protein FLJ22056
510575	0.5430211	hypothetical protein FLJ22087
810939	0.40256	hypothetical protein FLJ22169
2015517	0.5742448	hypothetical protein FLJ22237
1493218	-0.884795	hypothetical protein FLJ22297
1947381	0.3509235	hypothetical protein FLJ22329
37554	0.5706008	hypothetical protein FLJ22353
233679	-0.5356625	hypothetical protein FLJ22362
753378	0.548977	hypothetical protein FLJ22649 similar to signal peptidase SPC22/23
757328	0.3985331	hypothetical protein FLJ22678
244974	0.4105439	hypothetical protein FLJ22875
52103	0.4988158	hypothetical protein FLJ23045
161998	-0.5044691	hypothetical protein FLJ23138
1417886	-0.4941304	hypothetical protein FLJ23239
220395	-0.6418175	hypothetical protein FLJ23293 similar to ARL-6 interacting protein-2
1632247	0.3312131	hypothetical protein FLJ23436
455275	0.3869874	hypothetical protein FLJ23469
1651906	-0.5863631	hypothetical protein FLJ23544
144880	0.5704416	hypothetical protein from EUROIMAGE 1759349
1696757	0.5254296	hypothetical protein KIAA1165
625693	0.5055986	hypothetical protein MGC10911
131566	0.3261265	hypothetical protein MGC11061
781342	0.4716127	hypothetical protein MGC11115
824879	0.7432221	hypothetical protein MGC11275
773373	-0.6730112	hypothetical protein MGC14258
325606	0.647638	hypothetical protein MGC14353
240752	-0.56913	hypothetical protein MGC14797
1898619	0.4916939	hypothetical protein MGC15737
68636	0.6838604	hypothetical protein MGC2477
743810	0.3667087	hypothetical protein MGC2577
490023	-1.2114805	hypothetical protein MGC2648
815501	0.3214849	hypothetical protein MGC2721
1869201	0.6727191	hypothetical protein MGC2745



1558642	0.4298376	hypothetical protein MGC2771
773487	-0.5686324	hypothetical protein MGC3032
51773	0.6925666	hypothetical protein MGC3077
37708	0.6986007	hypothetical protein MGC3101
814443	-0.8385965	hypothetical protein MGC3232
1570427	-0.5280955	hypothetical protein MGC4309
42408	0.725109	hypothetical protein MGC4604
123614	0.633308	hypothetical protein MGC4675
120271	0.4886584	hypothetical protein MGC4692
120271	0.5982507	hypothetical protein MGC4692
812238	1.0043787	hypothetical protein MGC4692
1858892	0.6904662	hypothetical protein MGC4825
245485	0.3215041	hypothetical protein MGC5178
121251	0.385792	hypothetical protein MGC5576
293727	0.4242722	hypothetical protein MGC861
1597813	-0.5406089	hypothetical protein PP1044
810609	0.4551167	hypothetical protein PP1226
782501	-0.7086066	hypothetical protein PP1665
745606	1.1825585	hypothetical protein PP591
2028949	0.5946445	hypothetical protein PRO1855
701115	0.3936994	hypothetical protein PRO2013
815835	0.3764754	hypothetical protein R33729_1
625399	-0.9066615	hypothetical protein similar to beta-transducin family
238907	-0.5534598	hypothetical protein, clone Telethon(Italy_B41)_Strait02270_FL142
897806	0.6015789	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
39884	0.7075527	IMP (inosine monophosphate) dehydrogenase 1
1846982	0.3602851	inhibin, beta C
221295	0.5157877	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
788234	-1.3761312	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
505243	-0.6671218	inositol 1,4,5-triphosphate receptor, type 2
703964	-0.5620699	inositol polyphosphate phosphatase-like 1
180803	-0.621787	inositol polyphosphate-1-phosphatase
77533	0.3205713	inositol polyphosphate-5-phosphatase, 40kD
207288	0.603346	insulin induced gene 1
814350	0.588877	insulin-degrading enzyme
753620	-0.5248489	insulin-like growth factor binding protein 6
471196	-0.7192268	integral membrane protein 3
785530	-0.5600048	integrin, alpha 1
188388	-0.6824191	integrin, alpha 10



32493	-0.7093777	integrin, alpha 6
130201	-1.0401997	intercellular adhesion molecule 2
755599	0.3413351	interferon induced transmembrane protein 1 (9-27)
1159963	0.4323117	interferon regulatory factor 7
782513	0.4759571	interferon, alpha-inducible protein (clone IFI-6-16)
824602	-0.5107682	interferon, gamma-inducible protein 16
154493	0.3629466	interferon-induced protein 75, 52kD
84295	0.3989864	interleukin 1 receptor antagonist
491763	-0.679034	interleukin 1, beta
811920	-1.2690713	interleukin 11 receptor, alpha
1517171	0.5195255	interleukin 2 receptor, alpha
80344	-0.8243418	interleukin 7 receptor
859228	0.5817344	isocitrate dehydrogenase 1 (NADP+), soluble
869375	0.4827093	isocitrate dehydrogenase 2 (NADP+), mitochondrial
868128	0.7347171	JM4 protein
414992	0.420994	K562 cell-derived leucine-zipper-like protein 1
344588	-0.55146	kallikrein 5
809784	-0.7095414	kallikrein 6 (neurosin, zyme)
2243051	-0.7736287	kallikrein 8 (neuropsin/ovasin)
824962	0.4638758	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
852829	0.3691079	karyopherin alpha 3 (importin alpha 4)
625234	0.550211	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
1474900	-0.736252	keratin 15
344988	0.3464047	<b>keratin, hair, acidic, Homo sapiens</b>
773922	0.6730903	KIAA0005 gene product
686172	0.6724684	KIAA0008 gene product
1350439	-0.6740833	KIAA0015 gene product
788444	0.4042598	KIAA0033 protein
814054	0.7539407	KIAA0040 gene product
725223	0.4167519	KIAA0077 protein
898032	0.7216	KIAA0097 gene product
841501	0.4111707	KIAA0102 gene product
530310	0.4739401	KIAA0143 protein
415191	-0.512457	KIAA0161 gene product
812975	-0.6921755	KIAA0172 protein
79710	0.4579008	KIAA0174 gene product
1517595	0.3804132	KIAA0175 gene product
43977	0.3961848	KIAA0182 protein
1473471	-0.9623482	KIAA0194 protein
49117	0.4856399	KIAA0215 gene product

1584287	0.4413331	KIAA0241 protein
782428	0.701077	KIAA0250 gene product
1884404	0.5849803	KIAA0285 gene product
2028238	-0.6141182	KIAA0300 protein
809944	0.6530236	KIAA0310 gene product
795805	0.4370764	KIAA0332 protein
773426	0.3727398	KIAA0391 gene product
752668	-0.65723	KIAA0440 protein
221499	0.4149929	KIAA0508 protein
1910316	0.3498986	KIAA0535 gene product
753162	-0.7617972	KIAA0603 gene product
725841	0.561197	KIAA0662 gene product
1636166	-0.8845211	KIAA0668 protein
180785	0.322529	KIAA0726 gene product
786265	0.3760397	KIAA0750 gene product
40173	0.5940582	KIAA0807 protein
460126	-0.5320146	KIAA0819 protein
26171	0.3656147	KIAA0856 protein
35300	-0.688788	KIAA0869 protein
1679942	0.3706798	KIAA1053 protein
277044	-0.6947855	KIAA1183 protein
124447	0.6918546	KIAA1184 protein
771004	-0.5144276	KIAA1201 protein
1843843	0.3290269	KIAA1304 protein
1518402	0.5497179	KIAA1361 protein
345056	-0.6863529	KIAA1404 protein
788558	-0.5600825	KIAA1479 protein
843054	0.4637278	KIAA1533 protein
50586	-0.6794282	KIAA1545 protein
812959	-0.5591846	KIAA1638 protein
1881774	-0.5265891	KIAA1678
149539	0.4138942	KIAA1700
277571	-0.9841522	KIAA1706 protein
703541	-0.5534921	KIAA1858 protein
753038	-0.893161	kinesin family member C3
825606	0.335057	kinesin-like 1
769942	0.3810371	kinesin-like 4
343731	0.3962504	<b>Kruppel-like factor 2 (lung) (KLF2), Homo sapiens</b>
132711	-0.7962294	Kruppel-like factor 5 (intestinal)
280249	0.4096162	Kruppel-like factor 7 (ubiquitous)
280907	-0.7307519	Kruppel-type zinc finger protein
795178	-0.5169102	lactate dehydrogenase C
346545	-0.7887371	laminin, beta 1
460403	-0.5739604	laminin, gamma 2 (nicein (100kD), kalinin (105kD), BM600 (100kD), Herlitz junctional epidermolysis bullosa))

770355	0.5518948	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
767202	-1.0654145	latent transforming growth factor beta binding protein 2
897731	-0.6670507	latrophilin
199403	0.7754748	lectin, galactoside-binding, soluble, 8 (galectin 8)
774078	-0.6508021	leiomodulin 1 (smooth muscle)
60565	0.4659865	lethal giant larvae (Drosophila) homolog 2
470092	0.476018	like-glycosyltransferase
1160723	-0.5005952	LIM domain kinase 2
712829	-0.5797871	LIM domain only 2 (rhombotin-like 1)
2056139	-1.0673271	LIM domain protein
247616	-0.6585351	lipoma HMGIC fusion partner
1469377	-1.2127781	lipoma HMGIC fusion partner-like 2
868169	-0.5584677	lipoprotein lipase
810947	0.3833137	LIS1-interacting protein NUDE1, rat homolog
825296	0.4646099	low density lipoprotein receptor defect C complementing
490778	0.5932928	low molecular mass ubiquinone-binding protein (9.5kD)
341759	-0.5403406	lung type-I cell membrane-associated glycoprotein
150314	0.5114988	lysophospholipase I
826363	0.5823873	lysophospholipase II
840942	-0.6383764	major histocompatibility complex, class II, DP beta 1
1592530	-0.5918818	mammalian inositol hexakisphosphate kinase 2
366100	-0.6885372	matrilin 2
470393	-0.830751	matrix metalloproteinase 7 (matrilysin, uterine)
142586	0.4942961	MCT-1 protein
2069602	0.3539588	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)
346688	-0.5315035	melanoma inhibitory activity
200814	-1.4325283	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
296880	-0.6655878	membrane protein, palmitoylated 1 (55kD)
729975	0.7649717	meningioma expressed antigen 5 (hyaluronidase)
1472735	-0.5888169	metallothionein 1E (functional)
1518890	0.5314577	metallothionein-like 5, testis-specific (tesmin)
878406	0.4396935	metaxin 1

2014034	0.6620303	methylene tetrahydrofolate dehydrogenase (NAD <sup>+</sup> dependent), methenyltetrahydrofolate cyclohydrolase
124298	0.4922937	microsomal glutathione S-transferase 3
133518	-0.6817662	microtubule-associated protein, RP/EB family, member 2
564492	0.5626905	mitochondrial carrier homolog 2
491524	0.3785047	mitochondrial ribosomal protein L13
321354	0.3489273	mitochondrial ribosomal protein L15
2019223	0.5663073	mitochondrial ribosomal protein L17
788334	0.5347204	mitochondrial ribosomal protein L23
416436	0.3325571	mitochondrial ribosomal protein L24
417801	0.4112944	mitochondrial ribosomal protein L27
782608	0.6137782	<b>mitochondrial ribosomal protein L9</b>
782608	0.6978285	mitochondrial ribosomal protein L9
1909574	0.3900357	mitochondrial ribosomal protein S11
70201	-0.6675012	mitochondrial solute carrier
590774	0.5460342	mitogen-activated protein kinase 13
767641	-0.5881449	mitogen-activated protein kinase 8 interacting protein 2
1358393	-0.5090372	mitogen-activated protein kinase kinase 3
342349	-0.603487	mitogen-activated protein kinase kinase kinase 14
2326057	0.5310995	MLN51 protein
154707	0.3831976	MpV17 transgene, murine homolog, glomerulosclerosis
530093	0.3463461	myelin protein zero-like 1
611443	0.5432426	myoglobin
470128	-0.5253542	myosin IE
1473274	-1.1172693	myosin regulatory light chain 2, smooth muscle isoform
712314	0.3338146	myosin regulatory light chain interacting protein
629944	0.5273447	myosin VB
744944	0.4769116	myosin VI
841308	-0.9953716	myosin, light polypeptide kinase
840865	0.4666048	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)
1456348	0.6417276	N-acetylneuraminic acid phosphate synthase; sialic acid synthase
66599	0.3561699	N-acetyltransferase 1 (arylamine N-acetyltransferase)
1635681	0.6022549	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)
951216	0.4594172	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)

487733	0.5057167	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (8kD, AGGG)
487733	0.6262778	<b>NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (8kD, AGGG)</b>
753457	0.3515361	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)
358609	0.4071867	NADH dehydrogenase (ubiquinone) flavoprotein 3 (10kD)
172785	0.3493683	NAG-5 protein
1762111	0.4160469	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
76605	0.6484522	nesca protein
773381	0.3525581	N-ethylmaleimide-sensitive factor attachment protein, alpha
52076	0.3633002	neuroblastoma (nerve tissue) protein
838478	-1.1175047	neurocalcin delta
289428	-0.7270494	neurotrophic tyrosine kinase, receptor, type 2
877621	-1.1501074	nGAP-like protein
306798	-0.8718483	NGFI-A binding protein 1 (EGR1 binding protein 1)
199645	0.5334951	nicastrin
85840	-0.7754435	nicotinamide N-methyltransferase
811761	0.6045809	Nijmegen breakage syndrome 1 (nibrin)
269606	0.3228482	N-methylpurine-DNA glycosylase
825659	0.424655	N-myc downstream regulated
842863	0.3225116	N-myc downstream regulated
75859	-1.8328232	N-myc downstream-regulated gene 2
845363	0.4570873	non-metastatic cells 1, protein (NM23A) expressed in
726658	0.4446657	non-metastatic cells 3, protein expressed in
203003	0.5743416	non-metastatic cells 4, protein expressed in
131091	0.3548154	Not56 (D. melanogaster)-like protein
789382	-0.6898974	Notch (Drosophila) homolog 4
795256	0.5567908	NPD007 protein
754040	-0.610807	NS1-associated protein 1
42831	0.3638165	N-terminal kinase-like
1637516	0.325364	nuclear autoantigen
703739	0.392298	nuclear cap binding protein subunit 1, 80kD
207794	0.3679245	nuclear factor (erythroid-derived 2), 45kD
345069	0.3532976	nuclear factor (erythroid-derived 2)-like 3
416959	-0.957248	nuclear factor I/B

503851	0.5170168	nuclear receptor co-repressor/HDAC3 complex subunit
823714	-0.642903	nuclear receptor co-repressor/HDAC3 complex subunit
773188	0.5454398	nuclear receptor subfamily 1, group D, member 2
377384	0.4698441	nuclear receptor subfamily 2, group F, member 2
815794	0.3643266	nucleobindin 2
1600281	0.3304323	nucleolar protein 3 (apoptosis repressor with CARD domain)
843070	-0.6925728	nucleoporin 88kD
811808	0.326728	nucleoside diphosphate kinase type 6 (inhibitor of p53-induced apoptosis-alpha)
42681	-0.5388424	NY-REN-25 antigen
773674	0.4601667	oncogene TC21
1523225	0.4195302	oncostatin M receptor
504461	0.3506753	opsin 3 (encephalopsin)
155896	-0.5182247	ORF
66535	0.5363248	ornithine decarboxylase antizyme 2
1533710	-0.5988282	ortholog of mouse integral membrane glycoprotein LIG-1
2028722	-0.8800075	osteoblast specific factor 2 (fasciclin I-like)
1753497	0.409432	ovo (Drosophila) homolog-like 1
111362	0.4045961	<b>oxysterol binding protein-like 2 (OSBPL2),</b>
756442	0.5313744	P450 (cytochrome) oxidoreductase
781019	0.5918462	paraoxonase 2
81203	0.3328573	paraoxonase 3
1404774	-0.5685596	parathyroid hormone-like hormone
785368	0.3254362	PDZ-binding kinase; T-cell originated protein kinase
1882697	-1.4318896	peanut (Drosophila)-like 2
416676	-0.9140494	pellino (Drosophila) homolog 1
285377	-1.3699153	pellino (Drosophila) homolog 2
1631132	0.401216	peptide transporter 3
1631682	-0.5162406	peptidylprolyl isomerase E (cyclophilin E)
1587710	-0.8252065	period (Drosophila) homolog 1
1573251	0.6410435	peroxisomal long-chain acyl-coA thioesterase
788518	-0.5697316	peroxisomal membrane protein 3 (35kD, Zellweger syndrome)
814353	0.3622592	phorbol-12-myristate-13-acetate-induced protein 1
897963	-0.9775616	phosphatidic acid phosphatase type 2A
85394	-0.4913773	phosphatidic acid phosphatase type 2B
346942	0.4657601	phosphatidylinositol glycan, class Q



788136	-0.7778375	phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)
773685	0.4009493	phosphodiesterase 4D interacting protein (myomegalin)
625923	0.5839066	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
897177	0.3712716	phosphoglycerate mutase 1 (brain)
712401	-0.9068788	phosphoinositide-3-kinase, catalytic, delta polypeptide
811779	-0.5291718	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)
811142	0.3361932	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
272529	0.7486269	phosphomannomutase 2
725284	0.4992842	phosphorylase kinase, gamma 2 (testis)
1474337	-0.7766266	phosphorylase, glycogen; brain
843195	0.8603524	phosphoserine phosphatase
503215	0.9108688	pilin-like transcription factor
586803	-0.7423407	placental growth factor, vascular endothelial growth factor-related protein
814815	-0.5675649	plakophilin 4
66491	-0.9280245	plasmolipin
1568391	-0.5467858	plastin 3 (T isoform)
810124	0.6162712	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)
52096	-0.6789228	platelet-derived growth factor receptor, alpha polypeptide
365358	0.5883524	pM5 protein
290378	-0.7751825	podocalyxin-like
859761	0.6573769	poliovirus receptor-related 2 (herpesvirus entry mediator B)
744047	0.4151137	polo (Drosophila)-like kinase
75059	-0.5504962	poly(A)-binding protein, cytoplasmic 1-like
897813	0.4749348	polyadenylate binding protein-interacting protein 1
741769	0.3475255	polymerase (DNA directed), beta
810734	0.4998276	polymerase (DNA-directed), delta 4
813410	0.5513568	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)
1325816	0.4379227	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)
814270	0.3300091	polymyositis/scleroderma autoantigen 1 (75kD)
756708	-0.910505	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4
67741	-1.0705249	PP2135 protein

69002	-0.9960916	PPAR(gamma) angiopoietin related protein
241348	0.7324115	prenylcysteine lyase
284592	-0.5205573	PRO1659 protein
280375	0.8392836	PRO2000 protein
263013	0.3894536	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2
2020898	0.4797032	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
486110	0.4017126	profilin 2
41698	0.4310061	progesterone binding protein
2161427	0.3509243	progesterone receptor
837864	0.3314764	progestin induced protein
1573946	0.5173691	programmed cell death 9
470035	0.3436575	prokineticin 1 precursor
138788	0.5302936	prolactin receptor
837870	-0.657186	proline arginine-rich end leucine-rich repeat protein
855800	0.4748367	prolyl endopeptidase
27544	-0.708383	prominin (mouse)-like 1
2213824	-0.5412089	protease inhibitor 3, skin-derived (SKALP)
307687	-0.5106552	protease, serine, 16 (thymus)
810558	0.6698194	proteasome (prosome, macropain) 26S subunit, ATPase, 4
2050827	0.5544641	proteasome (prosome, macropain) 26S subunit, ATPase, 5
1553306	0.5344506	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
823598	0.9153521	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
2054635	0.7914755	proteasome (prosome, macropain) subunit, alpha type, 7
122241	0.7394284	proteasome (prosome, macropain) subunit, beta type, 2
951233	0.5767874	proteasome (prosome, macropain) subunit, beta type, 3
1460110	0.5392177	proteasome (prosome, macropain) subunit, beta type, 5
1473289	0.674396	protective protein for beta-galactosidase (galactosialidosis)
26883	0.4103824	protein kinase (cAMP-dependent, catalytic) inhibitor beta
591055	-0.5258289	protein kinase C and casein kinase substrate in neurons 2
755301	0.3749416	protein kinase C, delta
2055807	0.5460123	protein kinase domains containing protein similar to phosphoprotein C8FW

205049	0.5734444	protein kinase H11; small stress protein-like protein HSP22
756666	0.4835569	protein phosphatase 1, catalytic subunit, alpha isoform
814989	0.3426862	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
41356	0.4746307	protein phosphatase 2, regulatory subunit B (B56), alpha isoform
358162	0.4901786	protein predicted by clone 23627
785707	0.4708376	protein regulator of cytokinesis 1
73638	0.3425644	protein tyrosine phosphatase type IVA, member 2
774502	0.3402891	protein tyrosine phosphatase, non-receptor type 12
83363	0.6526164	protein-L-isoaspartate (D-aspartate) O-methyltransferase
26566	-0.7278186	protein-O-mannosyltransferase 1
303109	-0.9414602	purinergic receptor (family A group 5)
141852	0.4748862	purinergic receptor P2Y, G-protein coupled, 2
1917941	0.8340565	purine-rich element binding protein B
744374	0.4824256	putative ankyrin-repeat containing protein
685516	0.8762873	putative G protein-coupled receptor
122077	0.9021901	putative membrane protein
261472	0.4941066	putative nuclear protein ORF1-FL49
795498	0.4270889	putative transmembrane protein
80374	-0.5236475	pyruvate dehydrogenase (lipoamide) alpha 1
826077	0.4242762	pyruvate dehydrogenase (lipoamide) beta
365060	0.4976091	RAB11A, member RAS oncogene family
79520	0.6769129	RAB2, member RAS oncogene family
1911343	0.9116745	RAB26, member RAS oncogene family
1639531	0.4658349	RAB27A, member RAS oncogene family
248886	-0.5823315	rab3 GTPase-activating protein, non-catalytic subunit (150kD)
784150	0.4702303	RAB31, member RAS oncogene family
785701	0.5446211	RAB31, member RAS oncogene family
1845169	0.5588842	RAB35, member RAS oncogene family
2009779	0.420743	rabaptin-5
687990	-0.5253354	Rac/Cdc42 guanine exchange factor (GEF) 6
470124	0.6641768	RAD1 (S. pombe) homolog
1476053	0.5179015	RAD51 (S. cerevisiae) homolog (E coli RecA homolog)
1686766	-0.7192745	Rag D protein
505864	-0.7677235	RalGDS-like gene
143426	0.3764075	ras homolog gene family, member B
2316441	-0.6206597	ras homolog gene family, member C

725308	-0.6371261	ras inhibitor
80727	-0.7538606	receptor tyrosine kinase-like orphan receptor 1
45099	-1.3515907	regucalcin (senescence marker protein-30)
2106144	-1.067765	regulated in glioma
1500542	0.3228485	regulator of G-protein signalling 11
813707	0.410787	regulator of G-protein signalling 16
2017403	0.3211799	regulator of G-protein signalling 3
383501	-0.502319	regulator of G-protein signalling 9
309288	0.334016	replication factor C (activator 1) 4 (37kD)
204299	0.4073087	replication protein A3 (14kD)
898253	0.3331924	reticulocalbin 2, EF-hand calcium binding domain
685185	-0.5172158	reticulon 2
781097	0.7126945	reticulon 3
2322367	0.5832711	reticulon 4
595037	0.990461	retinoic acid induced 3
756372	-0.5447652	retinoic acid receptor responder (tazarotene induced) 2
812994	0.4854155	retinoid X receptor, alpha
810959	0.3534647	Rho GDP dissociation inhibitor (GDI) alpha
244801	0.8066357	Rho guanine exchange factor (GEF) 11
1422338	0.5874097	ribonucleotide reductase M2 polypeptide
869450	-0.7659922	ribosomal protein L11
990881	-0.8335353	<b>ribosomal protein L12 (Rpl12), mus musculus</b>
814316	-0.9276916	ribosomal protein L13
307029	-0.6500872	ribosomal protein L26
1630990	-0.7312981	ribosomal protein L29
322561	-0.7970805	ribosomal protein L31
178137	-0.6839022	ribosomal protein L34
877835	-0.5382125	ribosomal protein L35
415233	-0.6506593	ribosomal protein L37a
51981	-0.5554908	ribosomal protein L7a
123441	0.4862068	ribosomal protein L7a
2252417	-0.6222381	ribosomal protein S10
772898	0.372064	ribosomal protein S15a
868308	-0.5157133	ribosomal protein S23
1637296	-0.5105214	ribosomal protein S24
1475738	-0.6753091	ribosomal protein S25
877827	-0.7093855	ribosomal protein S27a
1492147	-0.636656	ribosomal protein S4, X-linked
309449	-0.5401954	ribosomal protein S4, Y-linked
322233	-0.5578912	ribosomal protein, large, P0
469686	0.8919992	Ric (Drosophila)-like, expressed in many tissues

1636844	0.3926235	ring finger protein 14
200144	0.4019827	ring-box 1
133236	-0.8888316	RNA binding motif protein, X chromosome
746373	-0.5513143	RNA polymerase I transcription factor RRN3
813845	0.3637519	RNA, U transporter 1
291478	-1.0212528	runt-related transcription factor 3
756595	0.395121	S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
810612	0.6341098	S100 calcium-binding protein A11 (calgizzarin)
824108	0.3381616	SCAN domain-containing 1
416434	-0.8006527	SCN Circadian Oscillatory Protein (SCOP)
785840	0.5401209	SEC24 ( <i>S. cerevisiae</i> ) related gene family, member D
358456	0.4812268	Sec61 gamma
2306987	0.4402912	secreted and transmembrane 1
270917	-0.6918383	secreted frizzled-related protein 1
250654	-0.5815576	secreted protein, acidic, cysteine-rich (osteonectin)
2284803	-0.6265431	secretory carrier membrane protein 1
878836	-1.037352	secretory granule, neuroendocrine protein 1 (7B2 protein)
378813	-0.7346408	secretory leukocyte protease inhibitor (antileukoproteinase)
840878	0.5648009	seladin-1
1609625	-0.5920312	selectin P ligand
1492463	0.8634521	selenoprotein X, 1
327432	-0.4870045	semaphorin Y
207735	-0.7167416	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
592801	0.3638731	serine palmitoyltransferase, long chain base subunit 2
814378	0.6317382	serine protease inhibitor, Kunitz type, 2
209066	0.5794211	serine/threonine kinase 15
209066	0.6611038	<b>serine/threonine kinase 15</b>
271899	0.355689	Ser-Thr protein kinase related to the myotonic dystrophy protein kinase
161456	-0.8215502	serum amyloid A1
1917449	-1.0894686	serum amyloid A4, constitutive
159462	-0.528299	serum constituent protein
470061	0.77977	seven in absentia ( <i>Drosophila</i> ) homolog 2
813631	0.534683	seven transmembrane protein TM7SF3
49351	0.6386132	SEX gene
343760	-0.6724144	SH3 domain binding glutamic acid-rich protein like 2



2302099	0.5813788	sialidase 3 (membrane sialidase)
813751	0.5051993	sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase)
785616	0.6484744	signal sequence receptor, alpha (translocon-associated protein alpha)
2504881	-1.000863	signal transducer and activator of transcription 5A
144740	0.4449229	similar to phosphatidylcholine transfer protein 2
345034	-1.0600859	small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)
140574	-0.9652218	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)
2322223	0.3853156	small nuclear ribonucleoprotein polypeptide A
704414	0.6940045	small nuclear ribonucleoprotein polypeptides B and B1
288999	0.6938843	small protein effector 1 of Cdc42
1692195	0.3254467	smg GDS-ASSOCIATED PROTEIN
530958	-0.7809384	smoothened (Drosophila) homolog
810762	0.4806851	SNARE protein
472103	0.4043572	soc-2 (suppressor of clear, C.elegans) homolog
2054122	0.3318413	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3
755855	-0.6298333	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6
49273	0.5691181	solute carrier family 27 (fatty acid transporter), member 4
1568126	0.3434836	solute carrier family 37 (glycerol-3-phosphate transporter), member 1
1702742	0.5011725	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
289936	0.3382708	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
773286	0.3861543	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1
2413337	-0.4879268	sortilin-related receptor, L(DLR class) A repeats-containing
823871	-0.9429443	SPARC-like 1 (mast9, hevin)
815142	-0.4881454	spastic ataxia of Charlevoix-Saguenay (sacsin)
345764	-0.5504113	special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)



76362	0.3349202	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
1734309	0.5894492	sperm associated antigen 4
503866	0.4230404	sperm autoantigenic protein 17
565235	0.4124667	spermine synthase
1626304	-0.7769866	spinal cord-derived growth factor-B
813698	-0.4898644	sprouty (Drosophila) homolog 2
124781	0.6324418	squalene epoxidase
1558675	-1.3749762	SRY (sex determining region Y)-box 10
1469425	0.8296141	SRY (sex determining region Y)-box 22
768571	-0.8572018	SRY (sex determining region Y)-box 8
2306752	-0.5123647	stathmin-like 2
25440	0.3554359	staufer (Drosophila, RNA-binding protein) homolog 2
2018084	0.6119069	Ste-20 related kinase
302031	0.5111067	Ste20-related serine/threonine kinase
810711	0.9128832	stearoyl-CoA desaturase (delta-9-desaturase)
590759	0.4895021	sterol-C4-methyl oxidase-like
154466	0.3258377	STIP1 homology and U-Box containing protein 1
595070	0.3408109	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4
35191	0.3427094	stromal cell-derived factor 2
366132	1.013995	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD
125342	-0.5078237	SUMO-1-specific protease
781014	-1.0161379	suppression of tumorigenicity 5
785933	-0.5340762	sushi-repeat-containing protein, X chromosome
418159	-0.7545888	synaptogyrin 1
969877	0.707469	synaptosomal-associated protein, 25kD
177827	0.3691459	synaptotagmin VII
826194	0.4177687	synaptotagmin-like 2
135640	0.3288537	syntaxin 3A
509588	0.4157059	TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD
1474955	0.6045103	TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)
490102	-0.5383385	TBP-associated factor 172
366591	-0.7595643	T-cell lymphoma invasion and metastasis 2
726637	0.3292392	t-complex-associated-testis-expressed 1-like

1631194	0.3219004	t-complex-associated-testis-expressed 1-like 1
346696	0.3570344	TEA domain family member 4
47043	-0.7729643	tensin
454339	0.3738929	thiopurine S-methyltransferase
782193	-0.5788147	thioredoxin
795543	0.3500184	thioredoxin peroxidase (antioxidant enzyme)
789376	0.4339171	thioredoxin reductase 1
965223	0.3642603	thymidine kinase 1, soluble
739126	0.4905859	tissue specific transplantation antigen P35B
825470	0.5218731	topoisomerase (DNA) II alpha (170kD)
1591264	0.3849595	transaldolase 1
347373	0.7563599	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)
725680	-0.7197488	transcription factor AP-2 gamma (activating enhancer-binding protein 2 gamma)
713839	-0.5080365	transcription factor AP-4 (activating enhancer-binding protein 4)
823940	0.4214277	transducer of ERBB2, 1
1473131	-0.5594101	transducin-like enhancer of split 2, homolog of Drosophila E(sp1)
240248	-0.5660209	transferrin
705064	0.4497555	transforming, acidic coiled-coil containing protein 3
882248	-0.8700731	transgelin
878421	-0.5233873	transgelin 2
359887	0.8692353	translocase of inner mitochondrial membrane 17 (yeast) homolog A
149355	0.6520333	translocating chain-associating membrane protein
826256	0.7190206	transmembrane 7 superfamily member 1 (upregulated in kidney)
298417	0.3833014	trefoil factor 3 (intestinal)
855749	0.476968	triosephosphate isomerase 1
42076	0.3194462	TRK-fused gene
897720	-0.5904719	trophinin
740620	-0.96496	tropomyosin 2 (beta)
611532	-1.3158379	troponin I, skeletal, fast
1409509	0.554703	troponin T1, skeletal, slow
489657	0.3847527	tryptophan rich basic protein
757489	0.4859039	tubulin, alpha 2
825585	0.5722829	tubulin-specific chaperone e
1665444	-0.651994	tumor endothelial marker 1 precursor

142259	-0.8376566	tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcription factor IIIA-interacting protein
491403	-0.7700599	tumor necrosis factor receptor superfamily, member 1B
714213	-0.5129593	tumor necrosis factor receptor superfamily, member 6
814306	0.4705205	tumor protein D52
1435003	0.6457486	tumor suppressing subtransferable candidate 1
1856063	-0.8833091	tweety (Drosophila) homolog 1
292996	0.36439	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
868396	-0.808677	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
626318	0.4529715	ubinnuclein 1
1908834	-0.7177051	ubiquitin A-52 residue ribosomal protein fusion product 1
769921	0.6464245	ubiquitin carrier protein E2-C
81599	0.3932769	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)
745083	0.4107735	ubiquitin specific protease 18
795288	-0.6528792	ubiquitin specific protease 4 (proto-oncogene)
250883	-0.7925068	ubiquitin-activating enzyme E1-like
1698036	0.5298397	ubiquitin-conjugating enzyme E2 variant 1
839682	0.5208954	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
843094	-0.5617478	ubiquitin-like 1 (sentrin)
289978	0.6308861	ubiquitin-like 4
713862	0.3965573	ubiquitin-protein isopeptide ligase (E3)
824524	0.4375695	UDP-galactose transporter related
150897	-0.6188264	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
139835	0.5253386	UDP-glucose dehydrogenase
809727	0.365892	unc-51 (C. elegans)-like kinase 1
284261	0.6890531	uncharacterized hematopoietic stem/progenitor cells protein MDS030
1471829	-0.7275378	uncharacterized hypothalamus protein HSMNP1
884498	0.4648731	uncharacterized hypothalamus protein HT012
236034	0.7039329	uncoupling protein 2 (mitochondrial, proton carrier)
783681	0.354881	upstream regulatory element binding protein 1

769600	0.4362014	uracil-DNA glycosylase 2
1912951	0.329484	uterine-derived 14 kDa protein
81336	0.4955353	uteroglobin
1631699	0.6027911	valosin-containing protein
855061	-0.5203046	vascular endothelial growth factor B
240620	-0.5065007	vascular Rab-GAP/TBC-containing
215000	-0.555725	vasoactive intestinal peptide receptor 1
810057	-0.6178096	vasoactive intestinal peptide receptor 1
202901	0.48608	vav 2 oncogene
855563	0.5059683	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
810316	0.3732635	very long-chain acyl-CoA synthetase; lipidosin
1161775	-0.7380353	villin 1
840511	-0.6341661	vimentin
358531	-0.5784457	v-jun avian sarcoma virus 17 oncogene homolog
71087	-0.8416951	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F
290866	-0.5467613	v-raf-1 murine leukemia viral oncogene homolog 1
322617	0.3623149	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)
193913	-0.6425581	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
784140	0.474314	WD repeat domain 15
731023	0.4853217	WD repeat domain 5
268946	0.5440003	WD40 protein Ciao1
2306221	0.4068933	wingless-type MMTV integration site family, member 10B
235986	0.338857	wingless-type MMTV integration site family, member 11
138189	0.9386802	Wolfram syndrome 1 (wolframin)
813281	0.7092607	WW domain-containing protein 1
795185	0.5276861	xenotropic and polytropic retrovirus receptor
813629	0.6549767	YME1 (S.cerevisiae)-like 1
147834	0.4412795	zinc finger protein 217
209537	-0.763749	zinc finger protein 221
82421	0.3506778	zinc finger protein 6 (CMPX1)

Table 5 (in alphabetical order)

CloneID	Weight	Description
770785	0.658751	1,2-alpha-mannosidase IC

1574058	0.9058211	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
713782	0.6552297	a disintegrin and metalloproteinase domain 15 (metargidin)
488505	0.7242619	accessory proteins BAP31/BAP29
823930	0.6738266	actin related protein 2/3 complex, subunit 1A (41 kD)
1473922	0.7399948	actin related protein 2/3 complex, subunit 3 (21 kD)
340558	0.7990715	actin related protein 2/3 complex, subunit 5 (16 kD)
210862	0.7483198	acyl-Coenzyme A oxidase 1, palmitoyl
343607	0.6510034	AD-015 protein
51532	0.7195798	ADP-ribosylation factor-like 6 interacting protein
712139	-1.1491129	ADP-ribosylation factor-like 7
46248	0.9628117	ADP-ribosyltransferase (NAD <sup>+</sup> ; poly (ADP-ribose) polymerase)
248631	-1.0784377	aminomethyltransferase (glycine cleavage system protein T)
208718	-1.0229324	annexin A1
1435862	0.723081	antigen identified by monoclonal antibodies 12E7, F21 and O13
2110511	0.7863117	artemin
377275	-1.3392122	ataxia-telangiectasia group D-associated protein
810725	0.7561061	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 21kD
796694	1.1580364	baculoviral IAP repeat-containing 5 (survivin)
1709791	0.8397779	BAI1-associated protein 1
1456701	0.6383709	B-cell CLL/lymphoma 9
2043167	0.8551193	BCL2-associated athanogene 3
1420370	0.7726877	biliverdin reductase B (flavin reductase (NADPH))
811024	0.6706275	bone marrow stromal cell antigen 2
1616253	0.7231756	breast carcinoma amplified sequence 1
754653	0.6277098	cadherin, EGF LAG seven-pass G-type receptor 3, flamingo (Drosophila) homolog
67765	0.7064266	carboxypeptidase M
509823	0.6982362	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
744417	0.6975761	carnitine acetyltransferase
72778	-1.3299927	caspase 7, apoptosis-related cysteine protease
1878409	-1.013872	catechol-O-methyltransferase

842994	0.7983201	cathepsin Z
377461	-1.3214357	caveolin 1, caveolae protein, 22kD
725454	0.9476507	CDC28 protein kinase 2
786067	0.7228184	cell division cycle 25B
415102	0.6562436	cell division cycle 25C
2017415	0.7281714	centromere protein A (17kD)
2108077	0.6796871	CGI-112 protein
753400	0.6633015	CGI-204 protein
811774	0.9014801	CGI-49 protein
624667	0.9336899	CGI-92 protein
884425	0.6608337	chaperonin containing TCP1, subunit 5 (epsilon)
1492426	0.8032542	chromosome 19 open reading frame 3
469383	0.6925975	chromosome 8 open reading frame 1
124331	0.7081481	cleavage and polyadenylation specific factor 5, 25. kD subunit
770992	0.693225	<b>contig C056172, human</b>
897770	0.715754	<b>contig C071196, human</b>
108425	0.7581954	<b>contig C076797, human</b>
119290	-1.025797	cortic al thymocyte receptor (X. laevis CTX) like
839736	-1.2337192	crystallin, alpha B
742595	0.6784804	cyclin-dependent kinase 5
700792	0.8005506	cyclin-dependent kinase inhibitor 3 (CDK2- associated dual specificity phosphatase)
1323448	1.1309009	cysteine-rich protein 1 (intestinal)
278531	0.6404612	cytochrome c oxidase subunit VIc
1601947	0.6297475	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
768064	0.6936336	cytochrome P450, subfamily I (aromatic compound- inducible), polypeptide 1
810156	0.6879064	deoxythymidylate kinase (thymidylate kinase)
1161564	-1.5877154	desmuslin
842980	0.762412	developmentally regulated GTP-binding protein 1
760299	-1.8441097	dickkopf (Xenopus laevis) homolog 3
742685	-1.248683	disabled (Drosophila) homolog 2 (mitogen- responsive phosphoprotein)
825740	0.6805157	DKFZp434J1813 protein
1635062	-0.9905245	DKFZP586A011 protein
2011515	0.6319712	DKFZP586B0923 protein
454896	0.6384516	DnaJ (Hsp40) homolog, subfamily A, member 2
593023	-1.0158099	dystrobrevin, beta
781017	-1.0125987	early growth response 2 (Krox-20 (Drosophila) homolog)



366834	0.629867	envoplakin
153760	-1.0340645	EphB1
811088	-1.140941	ephrin-B3
109863	0.683291	epithelial membrane protein 2
358267	0.6648183	EST, Moderately similar to AF119917 63 PRO2831 [H.sapiens]
160609	-1.0208819	ESTs
196435	-1.1475545	ESTs
344091	0.6818771	ESTs
365738	0.7152855	ESTs
564847	0.6770455	ESTs
564981	0.7745626	ESTs
754628	0.9061145	ESTs
757191	-1.0238476	ESTs
784105	0.6244805	ESTs
827171	0.7543905	ESTs
1257131	-0.9869928	ESTs
1500162	0.8155519	ESTs
1536006	0.6805004	ESTs
431505	0.6840493	ESTs, Highly similar to A31026 probable membrane receptor protein [H.sapiens]
289760	-1.2610055	ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]
593431	0.6422897	ESTs, Moderately similar to CEGT_HUMAN CERAMIDE GLUCOSYLTRANSFERASE [H.sapiens]
345670	-1.2805684	ESTs, Moderately similar to I59348 CCAAT binding transcription factor CBF subunit C - rat [R.norvegicus]
529843	-1.0698218	ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]
120749	0.7545697	ESTs, Moderately similar to KIAA1215 protein [H.sapiens]
160192	-1.4231519	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
73009	0.731401	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
2016908	0.969649	ESTs, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens]
488642	0.6541915	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
1640821	0.920874	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]

742707	0.8515067	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens]
2029173	1.0094499	ESTs, Weakly similar to N-WASP [H.sapiens]
743589	0.8514377	ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]
35147	1.2581066	ESTs, Weakly similar to unnamed protein product [H.sapiens]
488202	0.932881	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens]
796542	-1.4697418	ets variant gene 5 (ets-related molecule)
811837	-1.157587	eukaryotic translation elongation factor 1 alpha 1
811837	-1.2030392	<b>eukaryotic translation elongation factor 1 alpha 1</b>
752631	0.6473517	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
789012	0.8351735	fibulin 2
131839	-1.3048208	folate receptor 1 (adult)
52419	-1.2447753	Friedreich ataxia region gene X123
2309073	0.8484971	frizzled (Drosophila) homolog 5
298122	-1.3364021	frizzled (Drosophila) homolog 7
1393018	0.8376676	general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD )
741474	1.0870449	glucose phosphate isomerase
1609836	0.9886168	glutamate-ammonia ligase (glutamine synthase)
731044	0.8716644	glutaredoxin 2
344720	-1.6567437	glycophorin C (Gerbich blood group)
686552	0.9182272	golgi phosphoprotein 1
1556433	-1.0887923	GRO3 oncogene
796181	-1.2276581	growth arrest-specific 6
788654	0.7244749	<b>growth factor receptor-bound protein 2</b>
788654	1.2573483	growth factor receptor-bound protein 2
810063	0.6286184	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)
308466	0.771216	GTP-binding protein Sara
283919	1.2112507	H2A histone family, member L
488964	1.3447179	H2A histone family, member O
290841	1.1670252	H2B histone family, member A
1500000	1.2926116	H2B histone family, member B
430235	0.7162503	H2B histone family, member Q
471568	1.1673113	hematological and neurological expressed 1

1569187	-1.4872982	heparan sulfate (glucosamine) 3-O-sulfotransferase 4
770845	0.7068283	hexokinase 1
345787	0.6981453	highly expressed in cancer, rich in leucine heptad repeats
172517	0.7779159	hippocalcin-like 1
323780	-1.0027215	Homo sapiens cDNA FLJ11177 fis, clone PLACE1007402
1474424	0.7689082	Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328
212542	0.7585053	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321
270826	-0.9896888	Homo sapiens cDNA FLJ13329 fis, clone OVARC1001795
1492780	0.6923749	Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409
770675	0.6315109	Homo sapiens cDNA: FLJ21323 fis, clone COL02374
131094	0.7626373	Homo sapiens cDNA: FLJ21587 fis, clone COL06946
814528	0.7845635	Homo sapiens cDNA: FLJ22139 fis, clone HEP20959
753071	-1.2005994	Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
840266	-1.200789	Homo sapiens cDNA: FLJ22667 fis, clone HSI08385
727078	0.7184618	Homo sapiens cDNA: FLJ23602 fis, clone LNG15735
796723	0.9915885	Homo sapiens clone CDABP0014 mRNA sequence
488404	-1.0484323	Homo sapiens clone TUA8 Cri-du-chat region mRNA
743977	0.6729967	Homo sapiens mRNA for TL132
327506	0.6943362	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 327506
44292	0.831599	Homo sapiens mRNA; cDNA DKFZp434C107 (from clone DKFZp434C107)
1871116	-1.209237	Homo sapiens mRNA; cDNA DKFZp434C1714 (from clone DKFZp434C1714); partial cds
2016648	0.917373	Homo sapiens mRNA; cDNA DKFZp434N1728 (from clone DKFZp434N1728)
565319	1.2155833	Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DKFZp564B1264)

813265	-1.3632094	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)
486683	-1.1548164	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)
1461477	0.6300096	Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324)
1584540	-1.0933558	Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022)
132857	-1.280579	Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone DKFZp586N1323)
22917	-1.2164705	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)
1631735	0.6404771	Homo sapiens, clone IMAGE:3604336, mRNA, partial cds
292770	0.6609782	Homo sapiens, clone IMAGE:3627860, mRNA, partial cds
810002	-1.3553375	Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds
1492238	0.8804306	HSPC003 protein
796469	1.4207633	HSPC150 protein similar to ubiquitin-conjugating enzyme
470099	0.7443747	HT002 protein; hypertension-related calcium-regulated gene
178805	1.0513873	Human DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to Drosophila Scratch (Scrt), Slug and Xenopus Snail, a novel gene similar to Drosophila CG6762, STSs, GSSs and five CpG
811585	0.738212	huntingtin (Huntington disease)
1554549	1.2787033	hydroxyacyl glutathione hydrolase
813419	0.6951349	hydroxyacyl-Coenzyme A dehydrogenase, type II
256619	0.6797698	hydroxysteroid (17-beta) dehydrogenase 7
595213	0.8978322	hypothetical protein
785766	0.7476331	hypothetical protein
810402	0.6978141	hypothetical protein
811848	-1.2011809	hypothetical protein
489351	0.7422879	hypothetical protein DKFZp566J2046
66406	0.8888639	hypothetical protein DKFZp762E1312
292936	0.7154295	hypothetical protein FLJ10468

753299	0.9019921	hypothetical protein FLJ10504
504308	0.8199799	hypothetical protein FLJ10540
246800	0.6867481	hypothetical protein FLJ10803
343695	-1.002495	hypothetical protein FLJ10875
2052113	0.8477245	hypothetical protein FLJ10903
768570	0.732628	hypothetical protein FLJ11280
589232	0.6865999	hypothetical protein FLJ11506
489594	0.645574	hypothetical protein FLJ11565
41569	0.691145	hypothetical protein FLJ12650
785795	0.6683919	hypothetical protein FLJ12910
150003	0.8447372	hypothetical protein FLJ13187
1605426	0.8317254	hypothetical protein FLJ13352
248649	0.7210707	hypothetical protein FLJ13910
1554167	-1.3141843	hypothetical protein FLJ14529
1505038	1.3277637	hypothetical protein FLJ20171
502774	0.6807524	hypothetical protein FLJ20623
1636092	0.8841788	hypothetical protein FLJ20657
300632	-1.449587	hypothetical protein FLJ21044 similar to Rbig1
429799	0.8386406	hypothetical protein FLJ21939 similar to 5- azacytidine induced gene 2
510575	0.6295917	hypothetical protein FLJ22087
2015517	0.6441737	hypothetical protein FLJ22237
753378	0.7492212	hypothetical protein FLJ22649 similar to signal peptidase SPC22/23
144880	0.6902434	hypothetical protein from EUROIMAGE 1759349
1696757	0.6599512	hypothetical protein KIAA1165
824879	0.7333071	hypothetical protein MGC11275
325606	0.6225147	hypothetical protein MGC14353
1898619	0.6651268	hypothetical protein MGC15737
68636	0.6778817	hypothetical protein MGC2477
490023	-1.1020527	hypothetical protein MGC2648
1869201	0.8825788	hypothetical protein MGC2745
51773	0.8588635	hypothetical protein MGC3077
37708	0.7163849	hypothetical protein MGC3101
814443	-1.0250673	hypothetical protein MGC3232
120271	0.6562017	hypothetical protein MGC4692
812238	1.2664748	hypothetical protein MGC4692
1858892	0.9669022	hypothetical protein MGC4825
121251	0.6596925	hypothetical protein MGC5576
293727	0.6728542	hypothetical protein MGC861
745606	1.0663136	hypothetical protein PP591
2028949	0.8358024	hypothetical protein PRO1855
625399	-1.0594452	hypothetical protein similar to beta-transducin family

897806	0.7388301	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
39884	0.7526496	IMP (inosine monophosphate) dehydrogenase 1
221295	0.7342275	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
788234	-1.1061158	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
207288	0.7058528	insulin induced gene 1
130201	-1.2181641	intercellular adhesion molecule 2
782513	0.8030042	interferon, alpha-inducible protein (clone IFI-6-16)
84295	0.6876167	interleukin 1 receptor antagonist
811920	-1.5255258	interleukin 11 receptor, alpha
80344	-1.0602825	interleukin 7 receptor
869375	0.808792	isocitrate dehydrogenase 2 (NADP+), mitochondrial
868128	0.8970146	JM4 protein
824962	0.7238234	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
773922	0.7799164	KIAA0005 gene product
686172	0.846207	KIAA0008 gene product
814054	1.0130821	KIAA0040 gene product
898032	0.9547022	KIAA0097 gene product
530310	0.6682042	KIAA0143 protein
782428	1.0008279	KIAA0250 gene product
809944	0.7139515	KIAA0310 gene product
753162	-1.0119485	KIAA0603 gene product
124447	0.6363079	KIAA1184 protein
1518402	0.6378481	KIAA1361 protein
277571	-0.9977509	KIAA1706 protein
343731	0.6424907	<b>Kruppel-like factor 2 (lung) (KLF2), Homo sapiens</b>
280249	0.64759	Kruppel-like factor 7 (ubiquitous)
280907	-0.9932806	Kruppel-type zinc finger protein
770355	0.6829507	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
767202	-1.4573536	latent transforming growth factor beta binding protein 2
199403	1.0142329	lectin, galactoside-binding, soluble, 8 (galectin 8)
2056139	-1.3506352	LIM domain protein
1469377	-1.359583	lipoma HMGIC fusion partner-like 2
150314	0.739762	lysophospholipase I
826363	0.6322533	lysophospholipase II



200814	-1.8295958	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
729975	0.8385313	meningioma expressed antigen 5 (hyaluronidase)
1518890	0.6251884	metallothionein-like 5, testis-specific (tesmin)
2014034	0.9619198	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase
124298	0.7507816	microsomal glutathione S-transferase 3
564492	0.7301895	mitochondrial carrier homolog 2
491524	0.6424448	mitochondrial ribosomal protein L13
2019223	0.7893602	mitochondrial ribosomal protein L17
782608	0.698569	mitochondrial ribosomal protein L9
590774	0.657447	mitogen-activated protein kinase 13
1473274	-1.3200174	myosin regulatory light chain 2, smooth muscle isoform
629944	0.6950339	myosin VB
841308	-1.3246996	myosin, light polypeptide kinase
1456348	0.7401571	N-acetylneuraminic acid phosphate synthase; sialic acid synthase
76605	0.7376829	nesca protein
838478	-1.2349342	neurocalcin delta
877621	-1.1422087	nGAP-like protein
199645	0.769591	nicastatin
811761	0.7578696	Nijmegen breakage syndrome 1 (nibrin)
75859	-1.5303427	N-myc downstream-regulated gene 2
845363	0.714201	non-metastatic cells 1, protein (NM23A) expressed in
203003	0.6802818	non-metastatic cells 4, protein expressed in
416959	-1.0566462	nuclear factor I/B
503851	0.6291771	nuclear receptor co-repressor/HDAC3 complex subunit
773188	0.6448143	nuclear receptor subfamily 1, group D, member 2
756442	0.7016064	P450 (cytochrome) oxidoreductase
1882697	-1.715818	peanut (Drosophila)-like 2
416676	-1.0568729	pellino (Drosophila) homolog 1
285377	-1.4496786	pellino (Drosophila) homolog 2
1587710	-1.0209983	period (Drosophila) homolog 1
1573251	0.7816689	peroxisomal long-chain acyl-coA thioesterase
897963	-1.0075423	phosphatidic acid phosphatase type 2A
625923	0.8821749	phosphoenolpyruvate carboxykinase 2 (mitochondrial)

712401	-1.1218827	phosphoinositide-3-kinase, catalytic, delta polypeptide
272529	0.9423688	phosphomannomutase 2
843195	0.8606568	phosphoserine phosphatase
503215	0.8286483	pilin-like transcription factor
810124	0.8891272	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)
290378	-0.9932643	podocalyxin-like
859761	0.6846134	poliovirus receptor-related 2 (herpesvirus entry mediator B)
744047	0.6748419	polo (Drosophila)-like kinase
897813	0.6741253	polyadenylate binding protein-interacting protein 1
813410	0.7093173	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)
67741	-1.3014364	PP2135 protein
241348	0.757138	prenylcysteine lyase
280375	0.9793036	PRO2000 protein
41698	0.6327738	progesterone binding protein
810558	0.943041	proteasome (prosome, macropain) 26S subunit, ATPase, 4
2050827	0.7211304	proteasome (prosome, macropain) 26S subunit, ATPase, 5
1553306	0.7471557	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
823598	1.1425746	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
2054635	1.0613961	proteasome (prosome, macropain) subunit, alpha type, 7
122241	0.939204	proteasome (prosome, macropain) subunit, beta type, 2
951233	0.8614727	proteasome (prosome, macropain) subunit, beta type, 3
1460110	0.7559869	proteasome (prosome, macropain) subunit, beta type, 5
2055807	0.638184	protein kinase domains containing protein similar to phosphoprotein C8FW
205049	0.6231646	protein kinase H11; small stress protein-like protein HSP22
41356	0.6961169	protein phosphatase 2, regulatory subunit B (B56), alpha isoform
358162	0.6999211	protein predicted by clone 23627
785707	0.8176557	protein regulator of cytokinesis 1
83363	0.7435058	protein-L-isoaspartate (D-aspartate) O-methyltransferase
303109	-1.0807576	purinergic receptor (family A group 5)

1917941	1.1872008	purine-rich element binding protein B
685516	0.7378926	putative G protein-coupled receptor
122077	1.2576139	putative membrane protein
365060	0.6350631	RAB11A, member RAS oncogene family
79520	0.9457391	RAB2, member RAS oncogene family
1911343	0.9110591	RAB26, member RAS oncogene family
1639531	0.7033264	RAB27A, member RAS oncogene family
1845169	0.8131362	RAB35, member RAS oncogene family
470124	0.8347241	RAD1 (S. pombe) homolog
1476053	0.7367106	RAD51 (S. cerevisiae) homolog (E coli RecA homolog)
505864	-1.0033263	RalGDS-like gene
45099	-1.566311	regucalcin (senescence marker protein-30)
2106144	-1.1719133	regulated in glioma
813707	0.6814476	regulator of G-protein signalling 16
781097	0.9100493	reticulon 3
2322367	0.9859632	reticulon 4
595037	1.2486446	retinoic acid induced 3
812994	0.6420817	retinoid X receptor, alpha
244801	0.908481	Rho guanine exchange factor (GEF) 11
1422338	0.7690604	ribonucleotide reductase M2 polypeptide
869450	-0.9934083	ribosomal protein L11
990881	-1.0640807	<b>ribosomal protein L12 (Rpl12), mus musculus</b>
307029	-1.0497874	ribosomal protein L26
322561	-1.1270333	ribosomal protein L31
469686	0.9381847	Ric (Drosophila)-like, expressed in many tissues
291478	-1.0400846	runt-related transcription factor 3
810612	0.7419597	S100 calcium-binding protein A11 (calgizzarin)
785840	0.6800437	SEC24 (S. cerevisiae) related gene family, member D
2306987	0.6501071	secreted and transmembrane 1
878836	-1.2200837	secretory granule, neuroendocrine protein 1 (7B2 protein)
1492463	0.8360771	selenoprotein X, 1
814378	0.8015236	serine protease inhibitor, Kunitz type, 2
209066	0.8582298	serine/threonine kinase 15
209066	1.0066096	<b>serine/threonine kinase 15</b>
161456	-1.0220494	serum amyloid A1
1917449	-1.217371	serum amyloid A4, constitutive
470061	0.9920108	seven in absentia (Drosophila) homolog 2
49351	0.6551453	SEX gene
343760	-1.0803279	SH3 domain binding glutamic acid-rich protein like 2

2302099	0.6386686	sialidase 3 (membrane sialidase)
813751	0.7665427	sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase)
785616	0.6800658	signal sequence receptor, alpha (translocon-associated protein alpha)
2504881	-1.1674204	signal transducer and activator of transcription 5A
140574	-1.103064	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)
704414	0.8498631	small nuclear ribonucleoprotein polypeptides B and B1
288999	0.8593924	small protein effector 1 of Cdc42
810762	0.6371461	SNARE protein
49273	0.635859	solute carrier family 27 (fatty acid transporter), member 4
823871	-1.2090693	SPARC-like 1 (mast9, hevin)
1734309	0.666164	sperm associated antigen 4
124781	0.6809199	squalene epoxidase
1558675	-1.2313679	SRY (sex determining region Y)-box 10
1469425	0.8391993	SRY (sex determining region Y)-box 22
1476065	0.6783519	stathmin 1/oncoprotein 18
810711	1.1074523	stearoyl-CoA desaturase (delta-9-desaturase)
590759	0.672734	sterol-C4-methyl oxidase-like
366132	1.1440486	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD
781014	-1.2659158	suppression of tumorigenicity 5
969877	0.6564571	synaptosomal-associated protein, 25kD
509588	0.6903363	TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD
1474955	0.8573467	TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)
47043	-1.0841886	tensin
789376	0.6883473	thioredoxin reductase 1
825470	0.9274271	topoisomerase (DNA) II alpha (170kD)
1591264	0.6337293	transaldolase 1
347373	1.0454939	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)
705064	0.8401441	transforming, acidic coiled-coil containing protein 3
359887	1.1837896	translocase of inner mitochondrial membrane 17 (yeast) homolog A

149355	0.8134342	translocating chain-associating membrane protein
826256	0.7092586	transmembrane 7 superfamily member 1 (upregulated in kidney)
740620	-1.071175	tropomyosin 2 (beta)
611532	-1.3689616	troponin I, skeletal, fast
1409509	0.8339967	troponin T1, skeletal, slow
825585	0.741258	tubulin-specific chaperone e
814306	0.6963874	tumor protein D52
1435003	0.8311727	tumor suppressing subtransferable candidate 1
769921	0.9944462	ubiquitin carrier protein E2-C
839682	0.8696528	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
289978	0.7931469	ubiquitin-like 4
824524	0.6424419	UDP-galactose transporter related
236034	0.673506	uncoupling protein 2 (mitochondrial, proton carrier)
1631699	0.7115561	valosin-containing protein
810316	0.6323393	very long-chain acyl-CoA synthetase; lipidosin
731023	0.7032815	WD repeat domain 5
268946	0.6881593	WD40 protein Ciao1
138189	0.7953361	Wolfram syndrome 1 (wolframin)
813281	0.8016742	WW domain-containing protein 1
813629	0.7102574	YME1 (S.cerevisiae)-like 1